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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 16:44:13 ; Search time 4314.97 Seconds
 (without alignments)
 11614.23 Million cell updates/sec

Title: US-09-826-581-3
 Perfect score: 1722
 Sequence: 1 cttggccctcaatcaaga.....gatgagaggctcgggttggaa 1722

Scoring table: Oligo_NTC
 Gap_o 60.0 , Gape_{st} 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 15

Total number of hits satisfying chosen parameters: 696229

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :	GenBml1.*	Result No.	Score	Query Match Length	DB ID	Description
	1: gb_ba:*	c 1	1722	100.0	1722	6 AX281580 Sequence
	2: gb_htg:*	c 2	1670	97.0	152129	2 AC027416 Homo sapi
	3: gb_in:*	c 3	1479	85.9	206854	9 AC009974 Homo sapi
	4: gb_vii:*	c 4	168	9.8	1647	6 AX281582 Sequence
	5: em_ba:*	c 5	168	9.8	2109	6 AX099776 Sequence
	6: em_fun:*	c 6	168	9.8	2115	9 AX099802 Sequence
	7: em_hum:*	c 7	168	9.8	2115	6 AF214519 Homo sapi
	8: em_vii:*	c 8	168	9.8	2290	9 HSRA249977 Homo sapi
	9: em_in:*	c 9	57	3.3	106	11 G67375 AB98 Human
	10: em_mu:*	c 10	39	2.3	227724	2 AF336381 Mus muscu
	11: em_om:*	c 11	38	2.2	1867	6 AX099774 Sequence
	12: em_or:*	c 12	38	2.2	1873	4 AF214520 Sus scrof
	13: em_ov:*	c 13	38	2.2	1873	6 AX099800 Sequence
	14: em_pa:*	c 14	38	2.2	1873	6 AX198331 Sequence
	15: em_ph:*	c 15	38	2.2	1873	6 AX198333 Sequence
	16: em_pi:*	c 16	38	2.2	1873	6 AX198335 Sequence
	17: em_vii:*	c 17	38	2.2	1873	6 AX198337 Sequence
	18: em_sts:*	c 18	38	2.2	1873	6 AX198339 Sequence
	19: em_vii:*	c 19	38	2.2	2022	6 AX099804 Sequence
	20: em_sts:*	c 20	38	2.2	5868	4 AF214521 Sus scrof
	21: em_sts:*	c 21	35	2.0	146577	2 AC128070 Rattus no
	22: em_sts:*	c 22	35	2.0	190183	2 AC129703 Rattus no
	23: em_sts:*	c 23	35	2.0	192968	2 AC127107 Rattus no
	24: em_sts:*	c 24	29	1.7	192968	2 AC127107 Rattus no
	25: em_sts:*	c 25	25	1.5	186248	2 AC026021 Homo sapi
	26: em_sts:*	c 26	25	1.5	216197	9 HSUDJ37C10 AL045569 Human DNA
	27: em_sts:*	c 27	24	1.4	1328	10 RNAMPKGAM X955718 R. norvegicus
	28: em_sts:*	c 28	24	1.4	1550	10 RNAD2113 U42413 Rattus norv
	29: em_sts:*	c 29	24	1.4	5946	10 RATNESTIN M34394 Rat nestin
	30: em_sts:*	c 30	24	1.4	184288	2 AC129422 Rattus no
	31: em_sts:*	c 31	23	1.3	1194	9 AB046627 Macaca fa
	32: em_sts:*	c 32	23	1.3	81704	9 AL512353 Human DNA
	33: em_sts:*	c 33	23	1.3	82806	9 AC007111 Homo sapi
	34: em_sts:*	c 34	23	1.3	192180	2 AC023331 Homo sapi
	35: em_sts:*	c 35	23	1.3	196413	2 AC097269 Pan trogl
	36: em_sts:*	c 36	23	1.3	198172	2 AC009065 Homo sapi
	37: em_sts:*	c 37	23	1.3	239434	2 AC012171 Homo sapi
	38: em_sts:*	c 38	22	1.3	74615	2 AC128292 Rattus no
	39: em_sts:*	c 39	22	1.3	138312	9 AC026333 Homo sapi
	40: em_sts:*	c 40	22	1.3	238825	2 AC105847 Rattus no
	41: em_sts:*	c 41	21	1.2	2079	10 BC019836 Mus muscu
	42: em_sts:*	c 42	21	1.2	41680	10 AF040091 Mus muscu
	43: em_sts:*	c 43	21	1.2	58725	9 AC003988 Human PAC
	44: em_sts:*	c 44	21	1.2	63680	2 AC101117 Mus muscu
	45: em_sts:*	c 45	21	1.2	78215	2 AC105803 Rattus no

ALIGNMENTS

RESULT 1
 AX281580 LOCUS Sequence 3 from Patent WO0177305.
 DEFINITION AX281580 VERSION GI:16608831
 ACCESSION KEYWORDS human
 ORGANISM Homo sapiens
 SOURCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Andersson,L., Lutman,H. and Marklund,S.
 TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
 JOURNAL Patent: WO 0177305-A 3 18-OCT-2001;

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

Arexis AB (SE)		Location/Qualifiers	
FEATURES	source	base count	origin
Query Match	1. 0.1722	Score 1722; DB 6; Length 1722;	
Best Local Similarity	100.0%; Mismatches 0; Indels 0; Gaps 0;		
Matches 1722; Conservative 0;			
Qy 1 CCGGCCCTCATAGATAGAAAGCCCTTCTGCTCTGGCAACGGTGTGGCAG 60	Db 1 CCGGCCCTCATAGATAGAAAGCCCTTCTGCTCTGGCAACGGTGTGGCAG 60	Db 1 CCGGCCCTCATAGATAGAAAGCCCTTCTGCTCTGGCAACGGTGTGGCAG 60	Db 1 CCGGCCCTCATAGATAGAAAGCCCTTCTGCTCTGGCAACGGTGTGGCAG 60
Qy 61 CCTCTATGGCACGAGAACAGAGCTTCTGGTGAAGCTGGAGGTGGTGAAG 120	Db 61 CCTCTATGGCACGAGAACAGAGCTTCTGGTGAAGCTGGAGGTGGTGAAG 120	Db 61 CCTCTATGGCACGAGAACAGAGCTTCTGGTGAAGCTGGAGGTGGTGAAG 120	Db 61 CCTCTATGGCACGAGAACAGAGCTTCTGGTGAAGCTGGAGGTGGTGAAG 120
Qy 121 GGAGATGGGGGGTGAAGGGAGATCTTGTAAGGTTCTGGGGTGTATCTGATAT 180	Db 121 GGAGATGGGGGGTGAAGGGAGATCTTGTAAGGTTCTGGGGTGTATCTGATAT 180	Db 121 GGAGATGGGGGGTGAAGGGAGATCTTGTAAGGTTCTGGGGTGTATCTGATAT 180	Db 121 GGAGATGGGGGGTGAAGGGAGATCTTGTAAGGTTCTGGGGTGTATCTGATAT 180
Qy 181 ACACAAAGCTGGCTTCAAGCCAAAGCCAGGGCCACGGTGTGGAGAAAGTCATCC 240	Db 181 ACACAAAGCTGGCTTCAAGCCAAAGCCAGGGCCACGGTGTGGAGAAAGTCATCC 240	Db 181 ACACAAAGCTGGCTTCAAGCCAAAGCCAGGGCCACGGTGTGGAGAAAGTCATCC 240	Db 181 ACACAAAGCTGGCTTCAAGCCAAAGCCAGGGCCACGGTGTGGAGAAAGTCATCC 240
Qy 241 GGAGCTGCATGGCAGCTGGAGCCCTGGAGAATTCCTGGCTGAATTTCCTGGCTGAAGTCTGGCACATCTGGAGCCCTGG 300	Db 241 GGAGCTGCATGGCAGCTGGAGCCCTGGCTGAATTTCCTGGCTGAAGTCTGGCACATCTGGAGCCCTGG 300	Db 241 GGAGCTGCATGGCAGCTGGAGCCCTGGCTGAATTTCCTGGCTGAAGTCTGGCACATCTGGAGCCCTGG 300	Db 241 GGAGCTGCATGGCAGCTGGAGCCCTGGCTGAATTTCCTGGCTGAAGTCTGGCACATCTGGAGCCCTGG 300
Qy 301 ATGACCAAGCTGACACCTTCACTCGCTACTGCAATGGCTAGGG 360	Db 301 ATGACCAAGCTGACACCTTCACTCGCTACTGCAATGGCTAGGG 360	Db 301 ATGACCAAGCTGACACCTTCACTCGCTACTGCAATGGCTAGGG 360	Db 301 ATGACCAAGCTGACACCTTCACTCGCTACTGCAATGGCTAGGG 360
Qy 361 AGCAATGGGGAGGGAGAGAAAGCCACACTGGCTGGGGCTGCC 420	Db 361 AGCAATGGGGAGGGAGAGAAAGCCACACTGGCTGGGGCTGCC 420	Db 361 AGCAATGGGGAGGGAGAGAAAGCCACACTGGCTGGGGCTGCC 420	Db 361 AGCAATGGGGAGGGAGAGAAAGCCACACTGGCTGGGGCTGCC 420
Qy 421 ACTGTCCTGGCCACAGTCCCACCTGGCTGGGGCA 480	Db 421 ACTGTCCTGGCCACAGTCCCACCTGGCTGGGGCA 480	Db 421 ACTGTCCTGGCCACAGTCCCACCTGGCTGGGGCA 480	Db 421 ACTGTCCTGGCCACAGTCCCACCTGGCTGGGGCA 480
Qy 481 GGGGACTGACCTCAACCTGCCTCCACATGGCTGGGGCTGCC 540	Db 481 GGGGACTGACCTCAACCTGCCTCCACATGGCTGGGGCTGCC 540	Db 481 GGGGACTGACCTCAACCTGCCTCCACATGGCTGGGGCTGCC 540	Db 481 GGGGACTGACCTCAACCTGCCTCCACATGGCTGGGGCTGCC 540
Qy 541 CCTCCCTGGAGGATGCTGACATCACTGCACTGGCTGGACTACA 600	Db 541 CCTCCCTGGAGGATGCTGACATCACTGCACTGGCTGGACTACA 600	Db 541 CCTCCCTGGAGGATGCTGACATCACTGCACTGGCTGGACTACA 600	Db 541 CCTCCCTGGAGGATGCTGACATCACTGCACTGGCTGGACTACA 600
Qy 601 GGTCCCCCTGGTAGGAGTGGGGATACTTGGGACCCAGGGGGGGCG 660	Db 601 GGTCCCCCTGGTAGGAGTGGGGATACTTGGGACCCAGGGGGGGCG 660	Db 601 GGTCCCCCTGGTAGGAGTGGGGATACTTGGGACCCAGGGGGGGCG 660	Db 601 GGTCCCCCTGGTAGGAGTGGGGATACTTGGGACCCAGGGGGGGCG 660
Qy 661 AGGGGAGTCTCTGGAGGCTGCCATAGAACGCCACGCTTCTGACTCTGGAGST 720	Db 661 AGGGGAGTCTCTGGAGGCTGCCATAGAACGCCACGCTTCTGACTCTGGAGST 720	Db 661 AGGGGAGTCTCTGGAGGCTGCCATAGAACGCCACGCTTCTGACTCTGGAGST 720	Db 661 AGGGGAGTCTCTGGAGGCTGCCATAGAACGCCACGCTTCTGACTCTGGAGST 720
Qy 721 CTCTCGATGTCCTAGGTCAGTCCTATGAGATGAAACAAAGATGAGCTGGAG 780	Db 721 CTCTCGATGTCCTAGGTCAGTCCTATGAGATGAAACAAAGATGAGCTGGAG 780	Db 721 CTCTCGATGTCCTAGGTCAGTCCTATGAGATGAAACAAAGATGAGCTGGAG 780	Db 721 CTCTCGATGTCCTAGGTCAGTCCTATGAGATGAAACAAAGATGAGCTGGAG 780
Qy 781 GGTTGAGTGGGGAGGAAAGGAAAGGGCTGGTAGTGGCTGGAGCTTAAG 840	Db 781 GGTTGAGTGGGGAGGAAAGGAAAGGGCTGGTAGTGGCTGGAGCTTAAG 840	Db 781 GGTTGAGTGGGGAGGAAAGGAAAGGGCTGGTAGTGGCTGGAGCTTAAG 840	Db 781 GGTTGAGTGGGGAGGAAAGGAAAGGGCTGGTAGTGGCTGGAGCTTAAG 840
Qy 841 GTGGAGGATGGGGAGTGGGGATCTCTGGTAGTGGGACATAGGGACCTCG 900	Db 841 GTGGAGGATGGGGAGTGGGGATCTCTGGTAGTGGGACATAGGGACCTCG 900	Db 841 GTGGAGGATGGGGAGTGGGGATCTCTGGTAGTGGGACATAGGGACCTCG 900	Db 841 GTGGAGGATGGGGAGTGGGGATCTCTGGTAGTGGGACATAGGGACCTCG 900
Qy 901 GTGGCTGACGGAGGGAGGAAAGCTGGCTGGAGCTGGAGCTCCC 960	Db 901 GTGGCTGACGGAGGGAGGAAAGCTGGCTGGAGCTGGAGCTCCC 960	Db 901 GTGGCTGACGGAGGGAGGAAAGCTGGCTGGAGCTGGAGCTCCC 960	Db 901 GTGGCTGACGGAGGGAGGAAAGCTGGCTGGAGCTGGAGCTCCC 960

AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, J., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boughgaiter, B., Brown, A., Burkett, G., Campoman, A., Castle, A., Chobepel, Y., Coilangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Gallegos, J., Gardyns, S., Ginde, S., Goeyte, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Headford, A., Horton, L., Howland, J., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Llamazares, R., Landers, T., Lehoczky, J., Levine, R., Liou, C., Liu, G., Locke, K., McDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McFernan, K., McPheeetrs, R., Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testayre, S., Theodore, J., Tirrell, A., Travars, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A., and Zody, M.
JOURNAL	Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Jun 7, 2000 this sequence version replaced gi:7342115. All repeats were identified using RepeatMasker: http://ftp.genome.washington.edu/RM/RepeatMasker.html
TITLE	Direct Submission
FEATURES	<p>Center project name: U7458 Center clone name: 504_G_11 Summary Statistics Sequencing vector: M13; M77815; 100% of reads Chemistry: dye-terminator B/G Dye; 100% of reads Assembly program: Phrap; version 0.950731 Consensus quality: 135316 bases at least Q40 Consensus quality: 143284 bases at least Q30 Consensus quality: 146503 bases at least Q20 Insert size: 161000; agarose-fp Insert size: 19039; sum-of-contigs Quality coverage: 3.1 in Q20 bases; agarose-fp Quality coverage: 3.3 in Q20 bases; sum-of-contigs</p> <p>NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.</p> <p>1 1005: contig of 1005 bp in length * 1006 1105: gap of 100 bp * 1106 2402: contig of 1297 bp in length * 2403 2502: gap of 100 bp * 2503 383: contig of 1321 bp in length * 3824 3923: gap of 100 bp * 3924 5020: contig of 1097 bp in length * 5021 5120: gap of 100 bp * 5121 6161: contig of 1041 bp in length * 6162 6261: gap of 100 bp * 6262 7547: contig of 1286 bp in length * 7548 7647: gap of 100 bp * 7648 9983: contig of 2336 bp in length * 9984 10081: gap of 100 bp * 10084 12556: contig of 2473 bp in length * 12557 12656: gap of 100 bp * 12657 15043: contig of 2387 bp in length</p>
source	<p>1. 152129 Location/Qualifiers /organism="Homo sapiens" /db_xref="taxon:9606" /clone="RP11-504G11" /CloneID="RPCI-11 Human Male BAC"</p> <p>misc_feature 1..1005 /note="assembly_fragment" misc_feature 1106..2402 /note="assembly_fragment" misc_feature 2503..3823 /note="assembly_fragment" misc_feature 3924..5020 /note="assembly_fragment" misc_feature 5121..6161 /note="assembly_fragment" misc_feature 6262..7547 /note="assembly_fragment" misc_feature 7648..9983 /note="assembly_fragment" misc_feature 10084..12556 /note="assembly_fragment" misc_feature 12657..15043 /note="assembly_fragment" misc_feature 1544..17123 /note="assembly_fragment" misc_feature 17224..19466 /note="assembly_fragment"</p>

Db 35118 ACCTGGTCCCCATCCTAACCAAGGTTCCTGGCCGGCCCTTCCCTACCGCAC 35059
 Qy 1561 TATCCAAAGATTGGCATCGGACATCCGAGACTTGGCTGGTGCTGAGAGCACC 1620
 Db 35058 TATCCAAAGATTGGCATCGGACATCCGAGACTTGGCTGGTGAGACGCC 34999
 Qy 1621 CATTCTGACTGACTGACATTTGGACCGCCGTTGTCGACTGCCTGCTCAA 1680
 Db 34998 CATTCTGACTGACTGACATTTGGACCGCCGTTGACCTGCTGCTGCTCAA 34939
 Qy 1681 CGAATGTGGTACCCACCCCCAGGATGAGGGCTCGGGCTGG 1721
 Db 14938 CGAATGTGGTACCCACCCCCAGGATGAGGGCTCGGGCTGG 34898

RESULT 3

AC009974/C
ORGANISM Homo sapiens BAC clone RP1-459I19 from 2, complete sequence.
DEFINITION Homo sapiens BAC clone RP1-459I19 from 2, complete sequence.
ACCESSION AC009974
VERSION AC009974 .9
KEYWORDS HTG
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Authors Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Nature Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9841074
REFERENCE Authors Harris,A. and Corton,M.
TITLE The sequence of Homo sapiens BAC clone RP1-459I19
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 206854)
AUTHORS Waterston,R. H.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 206854)
AUTHORS Waterston,R. H.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 206854)
AUTHORS Waterston,R. H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108 USA
REFERENCE 6 (bases 1 to 206854)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Nov 8, 2001 this sequence version replaced gi:13431203.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center Code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0459I19

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP1-11 human BAC library was made from the blood of one male donor, as described by Osegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: PBACE3_6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP1-1077K22; the clone sequenced to the right is RP1-64705. Actual start of this clone is at base position 1 of RP1-459I19; actual end is at base position 206854 of RP1-459I19.

DATA FROM AC079810 AND AC079812

Data from AC079810 and AC079812 was used to finish this clone, AC009974. Polymorphisms have been identified between AC079812 and AC009974. A single plasmid region exists between 18812-38903. An unresolved tandem in the HERV SVA exists between 184320-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES

Source

1. 206854
 /organism="Homo sapiens"
 /db_xref="Taxon: 9606"
 /chromosome="2"
 /map="2"
 /clones="RP1-459I19"
 /clone_id="RPCI-11"
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 /note="match to EST AL567345 (NID:912922610)"
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 wa04910.x1"

DEFINITION	Homo sapiens mRNA for AMP-activated protein kinase gamma 3 subunit (AMPK gamma 3 gene).	SOURCE	Homo sapiens.
ACCESSION	AJ249977	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VERSION	AJ249977.1	KEYWORDS	1 (bases 1 to 106)
SOURCE	Human	REFERENCE	Robic,A., Jeon,J.-T., Rey,V., Amarger,V., Chardon,P., Loofit,C., Anderson,L., Gellin,J. and Milan,D.
ORGANISM	Homo sapiens	AUTHORS	Construction of a high-resolution RH map of human 2q35 region on TNG panel and comparison with physical map of porcine homologous region 15q25
REFERENCE	1 ('bases 1 to 2230)	TITLE	Unpublished (2001)
AUTHORS	Cheung,P.C., Salt,I.P., Davies,S.P., Hardie,D.G. and Carling,D.	JOURNAL	Contact: Annie ROBIC, Denis MILAN
TITLE	Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding	COMMENT	Génétique Cellulaire Institut National de Recherche agronomique (INRA) BP27, 31326 Castanet Tolosan, France
JOURNAL	Biochem. J. 346 Pt 3, 659-669 (2000)	REFERENCE	Tel: (33) 5 61 28 51 21
PUBMED	20164049	2 ('bases 1 to 2290)	Fax: (33) 5 61 28 53 08
PUBMED	10658692	AUTHORS	Email: arobic@oulouse.inra.fr
REFERENCE	Carling,D.	TITLE	Primer A: TGGGCATCGGCCACATTC Primer B: GACCACA GGCA GTGAGCA
JOURNAL	Direct Submission (12-OCT-1999) Carling D., Cellular Stress Group, MRC Clinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 0NN, UNITED KINGDOM	JOURNAL	PCR Profile:
FEATURES	Location/Qualifiers	Initial incubation: 94 degrees C for 4 min	
source	1 .. 2290 /organism="Homo sapiens"	Denaturation: 94 degrees C for 30 seconds	
gene	/db_xref="taxon:9606"	Annealing: 55 degrees C for 30 seconds	
CDS	22 .. 15000	Polymerization: 72 degrees C for 30 seconds	
	/gene="AMPK gamma 3"	PCR cycles: 33	
	22 .. 15000	Thermal cycler: Perkin Elmer 9600	
	/gene="AMPK gamma 3"	Protocol:	
	/function="AMP-activated protein kinase regulatory	Template: 25 ng	
	subunit"	Primer: each 0.5 μM	
	/codon_start=1	dNTPs: each 200 μM	
	/product="AMP-activated protein kinase gamma 3 subunit"	Tag Polymerase: 0.1 units/reaction	
	/protein_id="CAB65117_1"	Total Vol: 15 μl	
	/db_xref="GI: 6688201"	Buffer:	
	/translation="MEPGIEHALRRTPWSLSSLGSEHQEMSTLEQENSSWSPAVTS	MgCl2: 2 mM	
	SSEERIGKRRAKAALRWTKQSVEEGPPGQGEPRSPRAAETGLEATFPKTPTRPAQAA	KCl: 50 mM	
	DPAVGVTPTGTWDLPSDQTAASAGSSSDDDVQEAEPEWEECEBGLLERPAIC	Tris-HCl: 20 mM	
	LSRQPAFPKLGDQDLRKGAGAQYIMRFLEEHCDYDANATSSLVIFDTMLEIKAPFA	pH: 8.4	
	LAVGVRAPLWDISKOFVGMILTQPLVYDQVYIQLQKLTETWRELYLGQCFKPVLVSI		
	PSLQPSFLYRQTDLGITFDRDLAGVLETAPILTADIVFDRRVSALPVNECCQV		
	VGSLPPPSFLVTLAQTYNHLMSLQDLSLQVLPSPGIDPSGPEK."		
BASE COUNT	501 a 674 c 617 g 498 t	STs	Primers were defined on sequence AA178898 (cDNA). No intron.
ORIGIN		primer_bind	Location/Qualifiers
		16 a 28 c 33 g 27 t 2 others	1. 106 /organism="Homo sapiens" /clone lib="Human"
		BASE COUNT	1. >106 /db_xref="taxon: 9606"
		ORIGIN	
Query Match	9.8%	RESULT	10
Best Local Similarity	100.0%	LOCUS	AF336381/c
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Db	1024 GGTTCCTCGTGCCTGGCCCTCTAACGGACTATCCAAGATTGGCATCGGC 1083	VERSION	AF336381.1 GI:13507298
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REFERENCE	1	(bases 1 to 227724)	HLAAACCTYNNHLDMMVGFALRQPTCLEGVLSCQPHBTLGEVIDRIVREQVHRLVLYDE
AUTHORS	Rump,A.	Hayes,C., Brown,S.D.M. and Rosenthal,A.	
TITLE	Mouse chromosome 1 genomic sequence		
JOURNAL	Unpublished		
REFERENCE	2	(bases 1 to 227724)	
AUTHORS	Rump,A.		
TITLE	Direct Submission		
COMMENT	Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr.11, Jena 07745, Germany		
• NOTE: This is a working draft, sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.			
• This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.			
• 17869: contig of 17669 bp in length	1	17869: gap of unknown length	
• 17910	32746: contig of 14777 bp in length		
• 32747	32846: gap of unknown length		
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VERSION			
KEYWORDS			
ORGANISM	Sus scrofa		
	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Cetartiodactyla; Suina; Suidae; Sus.		
REFERENCE	1	(bases 1 to 1867)	
AUTHORS	Andersson,L., Loof,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.		
TITLE	Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof		
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Best Local Similarity 100.0%; Pred. No. 1.5e-08; Matches 38; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;	JOURNAL FEATURES SOURCE	Patent: WO 0220850-A 1 14-MAR-2002; Iowa State University Research Foundation, Inc. (US) Location/Qualifiers 1. -1873 /organism="Sus scrofa" /db_xref="taxon:9823" 1. -1395 /note="unnamed protein product" /codon_start=1 /protein_id="CAD3225_1"
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Search completed: January 7, 2003, 20:11:10
Job time : 4937.97 secs

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OM nucleic - nucleic search, using SW model

Run on: January 6, 2003, 17:17:03 ; Search time 479.092 Seconds
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SUMMARIES

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3	278	16.9	1014	10 US-09-826-581-4	Sequence 4, Appli
4	168	10.2	1722	10 US-09-826-581-3	Sequence 3, Appli
c 5	85	5.2	378	10 US-09-864-761-3373	Sequence 3373, Appli
c 6	54	3.3	92	10 US-09-864-761-20146	Sequence 20146, Appli
c 7	52	3.2	921	10 US-09-864-551-1	Sequence 1, Appli
c 8	20	1.2	333	10 US-09-974-300-1402	Sequence 1402, Appli
c 9	19	1.2	1411	9 US-09-935-720-2	Sequence 2, Appli
c 10	19	1.2	7771	9 US-09-832-292-38	Sequence 38, Appli
c 11	18	1.1	153	10 US-09-864-761-2801	Sequence 2201, Appli
c 12	18	1.1	325	10 US-09-960-352-2438	Sequence 2438, Appli
c 13	18	1.1	394	10 US-09-867-701-968	Sequence 968, Appli
c 14	18	1.1	459	10 US-09-864-761-0044	Sequence 6044, Appli
c 15	18	1.1	487	10 US-09-962-436-230	Sequence 220, Appli
c 16	18	1.1	487	10 US-09-880-107-1075	Sequence 1075, Appli
c 17	18	1.1	3364	10 US-09-919-497-18	Sequence 665, Appli
c 18	18	1.1	6746	10 US-09-967-768A-303	Sequence 18, Appli
c 19	18	1.1	6746	10 US-09-967-768A-303	Sequence 303, Appli

ALIGNMENTS

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; Sequence 5, Application US/09826581
; Patent No. US2003142310A1
; GENERAL INFORMATION:
;   APPLICANT: Andersson, Leif
;   APPLICANT: Luttmann, L. Holger
;   APPLICANT: Marklund, Stefan
;   TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
;   FILE REFERENCE: 11145-007001
;   CURRENT APPLICATION NUMBER: US/09/826,581
;   PRIORITY FILING DATE: 2001-04-05
;   PRIORITY NUMBER: US 60/195,665
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: FastSeq for Windows Version 4.0
;   SEQ ID NO 5
;   LENGTH: 1647
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;     NAME/KEY: CDS
;     LOCATION: (20) . . . (1486)
US-09-826-581-5

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Best Local Similarity 100.0%; Mismatches 0;
Matches 1647; Conservative 100.0%; Score 1647; DB 10; Length 1647;
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Db	661	GCCCTTCTTGTCTCTGGCCAAACGGTGTGGGAGGCCCTATGGACACAGAA 720	; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP- ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT ; CURRENT APPLICATION NUMBER: US/09/826-581		
Qy	721	CGAGAGCTTGTGGGATGCTGACCATGACTCTGGGTGTGATCGCTACTA 780	; CURRENT FILING DATE: 2001-04-05 ; PRIOR APPLICATION NUMBER: US1145100701		
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Qy	1081	CAACATCCGAGACTTGGCTGTGCTGAGACAGCACCCATCTGACTCGTGGACAT 1140	Qy	427	CACGGAGTTCCAGGCCAGGGCTGGGACTGTGAGCTGAGTGGCTGGAGAGAC 486
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 ; Patent No. US20020142310A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andersson, Leif
 ; Luthman, L. Holger
 ; APPLICANT: Stefan
 ; MARKLUND, Stefan
 ; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
 ; FILE REFERENCE: 11145-007001
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIORITY APPLICATION NUMBER: US/09/826-581
 ; PRIORITY FILING DATE: 2000-04-07
 ; NUMBER OF SEQ ID NOS: 14
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Query 1610 GCTCTGCCCTGGCCATGACCAAGCCCTCTAGCTTCACTGATGGTAG 1647
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RESULT 4
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 ; Sequence 3 Application US/09826581
 ; Patent No. US20020142310A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andersson, Leif
 ; Luthman, L. Holger
 ; APPLICANT: Stefan
 ; MARKLUND, Stefan
 ; TITLE OF INVENTION: VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT
 ; FILE REFERENCE: 11145-007001
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIORITY APPLICATION NUMBER: US 60/195, 665
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3

US-09-974-300-1402
 Sequence 1402, Application US/09374300
 GENERAL INFORMATION:
 APPLICANT: Berka, Randy M.
 TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 FILE REFERENCE: 10085_500-US
 CURRENT APPLICATION NUMBER: US/09/974,300
 CURRENT FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 09/680,598
 PRIOR FILING DATE: 2000-10-06
 PRIOR APPLICATION NUMBER: 60/279,526
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 8481
 SEQ ID NO: FastSEQ for Windows Version 4.0
 LENGTH: 313
 TYPE: DNA
 ORGANISM: Bacillus licheniformis
 US-09-974-300-1402

Qy 145 GACCAGCAGCTCAAGAAAGAA 164
 Db 265 GACCAGCAGCTCAAGAAAGAA 284

RESULT 9
 US-09-935-720-2
 Sequence 2, Application US/09335720
 Patent No. US200215260A1
 GENERAL INFORMATION:
 APPLICANT: HIRANO, TOSHIO
 TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS: PRE-B CELL GROWTH-SUPPORTING ABILITY
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/09/935,720
 FILING DATE: 24-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/517,739
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US/08/997,252
 FILING DATE: 23-DEC-1997
 APPLICATION NUMBER: US 08/537,142
 FILING DATE: 21-NOV-1995
 APPLICATION NUMBER: PCT/JP94/00819
 FILING DATE: 20-MAY-1994
 APPLICATION NUMBER: JP 5-141178
 FILING DATE: 21-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618

US-09-935-720-2
 Query Match 1.2%; Score 19; DB 9; Length 1411;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-832-292-38/c
 Sequence 38, Application US/09832292
 Patent No. US2002177205A1
 GENERAL INFORMATION:
 APPLICANT: Razaznov, Alexey
 TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
 SEQUENCES THEREOF
 FILE REFERENCE: 601-1-098CP
 CURRENT APPLICATION NUMBER: US/09/832,292
 CURRENT FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: 09/632,131
 PRIOR FILING DATE: 2001-08-03
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 38
 LENGTH: 7771
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-832-292-38

Query Match 1.2%; Score 19; DB 9; Length 7771;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-864-761-22801
 Sequence 22801, Application US/09864761
 Patent No. US200204863A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wenshang
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Acenica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04

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; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/234,667
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 22801
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003104.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EST HUMAN HIT: AW49933.1, EVALU=2.00e-71
; OTHER INFORMATION: NT HIT: gi|1426182, EVALU=1.00e-71
US-09-864-161-22801

Query Match 1.1%; Score 18; DB 10; Length 153;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 737 ATGCTGACCATCACTGAC 754
Db 96 ATGCTGACCATCACTGAC 113

RESULT 1.2
US-09-960-152-2438
; Sequence 2438, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Byatt, John C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Mathia Alagan, Nagappan
; TITLE OF INVENTION: NUCLEAR ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

; FILE REFERENCE: Aeomix-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312

; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO: 2438
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (240)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 11-LIB3058-018-Q1-K1-C3
US-09-960-352-2438

Query Match 1.1%; Score 18; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 CCTGCGAGGGAGGCC 231
Db 18 GGTGGAGGAAGGGAGGCC 35

RESULT 1.3
US-09-867-701-968/C
; Sequence 968, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Agigate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlock, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO: 968
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(394)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-968

Query Match 1.1%; Score 18; DB 10; Length 394;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1627 GACACCAGCCCTTTCATGC 1644
Db 38 GACACCAGCCCTTTCATGC 21

RESULT 1.4
US-09-864-761-6044
; Sequence 6044, Application US/0986476A1
; Patent No. US2002004876A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzei, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Gene Expression Analysis By Microarray
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312

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; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annotrax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 6044
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003104.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

RESULT 15
US-09-864-761-6044
; Sequence 230, Application US/0962436
; Parent No: US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Seq
; FILE REFERENCE: 609290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 20:16:02 ; Search time 62.0864 Seconds
 (without alignments)
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Title: US-09-826-581-5

Perfect score: 1647

Sequence: 1 ttgtctggggggccaca.....acaccaggcctttagtcttc 1647

Scoring table: OLIGO_NUC

Gapext: 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 15

Total number of hits satisfying chosen parameters: 737

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgtn2_6/.ptodata/2/ina/5A_COMB.seq;*
- 2: /cgtn2_6/.ptodata/2/ina/5B_COMB.seq;*
- 3: /cgtn2_6/.ptodata/2/ina/6A_COMB.seq;*
- 4: /cgtn2_6/.ptodata/2/ina/6B_COMB.seq;*
- 5: /cgtn2_6/.ptodata/2/ina/PCTUS_COMB.seq;*
- 6: /cgtn2_6/.ptodata/2/ina/backfiles.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	19	1.2	1411	1	US-08-537-942A-2	Sequence 2, Appli
2	19	1.2	1411	4	US-08-992-252A-2	Sequence 2, Appli
3	19	1.2	1411	4	US-09-511-739-2	Sequence 2, Appli
C 4	17	1.0	423	1	US-08-170-179-189	Sequence 189, Appli
5	17	1.0	1419	2	US-08-194-B-4	Sequence 4, Appli
6	17	1.0	1545	2	US-08-660-963-9	Sequence 9, Appli
7	17	1.0	1576	3	US-09-101-146-63	Sequence 63, Appli
8	17	1.0	1591	2	US-08-194-B-3	Sequence 3, Appli
9	17	1.0	1703	3	US-08-646-271-18	Sequence 18, Appli
10	17	1.0	1852	1	US-08-201-118-10	Sequence 10, Appli
11	17	1.0	1852	2	US-08-238-821-B-4	Sequence 10, Appli
12	17	1.0	1852	5	PCT-US95-05744-10	Sequence 10, Appli
13	17	1.0	1854	1	US-08-201-118-9	Sequence 4, Appli
14	17	1.0	1854	2	US-08-238-821B-4	Sequence 4, Appli
15	17	1.0	1854	5	PCT-US95-05744-4	Sequence 4, Appli
16	17	1.0	2129	3	US-08-646-273-22	Sequence 22, Appli
17	17	1.0	2314	3	US-08-646-273-29	Sequence 29, Appli
18	17	1.0	2707	2	US-08-709-874A-9	Sequence 9, Appli
19	17	1.0	2707	4	US-09-104-382-9	Sequence 9, Appli
20	17	1.0	2889	1	US-08-289-112-1	Sequence 1, Appli
21	17	1.0	2907	2	US-09-018-628-17	Sequence 17, Appli
22	17	1.0	2907	3	US-09-273-378-17	Sequence 17, Appli
23	17	1.0	2907	4	US-09-018-635-26	Sequence 3, Appli
24	17	1.0	2907	4	US-09-467-642-3	Sequence 1, Appli
25	17	1.0	3697	1	US-08-571-788-1	Sequence 1, Appli
26	17	1.0	3697	1	US-08-309-984A-1	Sequence 1, Appli
27	17	1.0	3697	1	US-08-309-983-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
 US-08-537-942A-2
 ; Sequence 2, Application US/08537942A
 ; Patent No. 5753364

GENERAL INFORMATION:

- / APPLICANT: HIRANO, TOSHIO
- / APPLICANT: KAIISHO, NISHINOMIYA
- / TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A PRE-B CELL GROWTH-SUPPORTING ABILITY
- / NUMBER OF SEQUENCES: 2
- / CORRESPONDENCE ADDRESS:
- / ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
- / ADDRESS: P.C.
- / STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
- / STATE: ARLINGTON
- / COUNTRY: VA
- / ZIP: 22202

COMPUTER READABLE FORM:

- / MEDIUM TYPE: Floppy disk
- / COMPUTER: IBM PC compatible
- / OPERATING SYSTEM: PC-DOS/MS-DOS
- / SOFTWARE: Patent in Release #1.0. Version #1.30
- / CURRENT APPLICATION DATA:
- / APPLICATION NUMBER: US/08/537,942A
- / FILING DATE: 21-NOV-1995
- / CLASSIFICATION: 435
- / PRIOR APPLICATION DATA:
- / APPLICATION NUMBER: PCT/JP94/00019
- / FILING DATE: 20-MAY-1994
- / PRIOR APPLICATION DATA:
- / APPLICATION NUMBER: JP 5-141178
- / FILING DATE: 21-MAY-1993
- / ATTORNEY/AGENT INFORMATION:
- / NAME: OBLON, NORMAN F.
- / REGISTRATION NUMBER: 24,618
- / REFERENCE/DOCKET NUMBER: 4767-004-0 PCT
- / TELECOMMUNICATION INFORMATION:
- / TELEPHONE: 703-413-3000
- / TELEFAX: 703-413-2220
- / INFORMATION FOR SEQ ID NO: 2:
- / SEQUENCE CHARACTERISTICS:
- / LENGTH: 1411 base pairs
- / TYPE: nucleic acid
- / STRANDEDNESS: double
- / TOPOLOGY: linear
- / MOLECULE TYPE: cDNA to mRNA
- / FEATURE:
- / NAME/KEY: sig_peptide
- / LOCATION: 1..84

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US-08-537-142A-2 OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
Query Match 1.2%; Score 19; DB 1; Length 14
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0

Qy 1112 ACAGACCCATCCTGACTG 1130
Db 948 ACAGACCCATCCTGACTG 966

RESULT 2
US-08-997-252A-2
Sequence 2, Application US/08997252A
Patient No. 6732453
GENERAL INFORMATION:
APPLICANT: HIRANO, TOSHIRO
APPLICANT: KAISHO, NISHINOMIYA
TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING PRE-B CELL GROWTH-SUPPORTING ABILITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: P. C. SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997-252A
FILING DATE: 23-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/537, 942
FILING DATE: 21-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00819
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-141178
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24, 618
REFERENCE DOCKET NUMBER: 4767-0005-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: sig peptide
LOCATION: 1..84
OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
US-08-997-252A-2
Query Match 1.2%; Score 19; DB 4; Length 14
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0

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Sequence 189, Application US/08470179
Patent No. 5645994

GENERAL INFORMATION:

APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Method and Computer Program Product for Identifying Sequences

NUMBER OF SEQUENCES: 207

CORRESPONDENCE ADDRESS:

ADDRESSEE: Trask, Britt and Ross
STREET: P.O. Box 2550
CITY: Salt Lake City
STATE: Utah
COUNTRY: USA

ZIP: 84110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: Patent in Release #1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,179
FILING DATE: 12-10-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Swiergent Ph.D, Susan E.
REGISTRATION NUMBER: 36,289
REFERENCE/DOCKET NUMBER: 2601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801-532-1922
TELEFAX: 801-531-9168

INFORMATION FOR SEQ ID NO: 189:

SEQUENCE CHARACTERISTICS:

LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Thermus thermophilus

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Query Match      1.0%; Score 17; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.1e+02
Matches 17; Conservative 0; Mismatches 0
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          61 GCGGGACCCGCTCTGG 45

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RESULT 5
IS-08-194-981E-4
Sequence 4, Application US/08194981E
Patent No. 5886157
GENERAL INFORMATION:
APPLICANT: GUENGERICH, F. Peter
APPLICANT: GUO, Zuyu
APPLICANT: SANDHU, Punam
APPLICANT: GILLAM, Elizabeth M. J.
TITLE OF INVENTION: EXPRESSION AND PURIFICATION
TITLE OF INVENTION: HUMAN
TITLE OF INVENTION: CYTOCHROME P450

NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street, NE
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent-In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/194,981E
 FILING DATE: February 10, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Selby
 REGISTRATION NUMBER: 38,298
 REFERENCE/DOCKET NUMBER: 220000.00022
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 688-0770
 TELEFAX: (404) 688-9880
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1419 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-194-981E-4

Query Match 1.0% ; Score 17; DB 2; Length 1419
 Best Local Similarity 100% ; Pred. No. 1.1e+02;
 Matches 17 ; Conservative 0 ; Mismatches 0;

Qy	1266	GTTGGGAGAACCCCTG	1282
Db	1250	GTTGGGAGAACCCCTG	1266

RESULT 6
 US-08-194-963-9
 Sequence 9, Application US/08660963
 Patent No. 5852187
 GENERAL INFORMATION:
 APPLICANT: Thorner, Michael O.
 ATTORNEY: Gaylinn, Bruce D.
 APPLICANT: Horikawa, Reiko
 APPLICANT: Lyons Jr., Charles E.
 TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE GROWTH HORMONE RELEASING HORMONE
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN,
 STREET: Metropolitan Square Building, Suite 800
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent-In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/660,963
 FILING DATE: 12-JUN-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: O'Shaughnessy, Brian P.
 REGISTRATION NUMBER: 32,747
 REFERENCE/DOCKET NUMBER: 18046.036
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-824-8000
 TELEFAX: 202-824-8199
 TELEX: 248516
 INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1545 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 NAME/KEY: CDS
 LOCATION: 1..1371

US-08-660-963-9

RESULT 8
 US-08-194-981E-3
 Sequence 3, Application US/08194981E
 Patent No. 5886157
 GENERAL INFORMATION:
 APPLICANT: GUENGERICH, F. Peter
 APPLICANT: GUO, Zuyu
 APPLICANT: SANDHU, Purnam
 APPLICANT: GILLAM, Elizabeth M. J.
 EXPRESSION AND PURIFICATION OF
 TOPIC OF INVENTION: HUMAN
 TITLE OF INVENTION: CYTOCHROME P450
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NEEDLE & ROSENBERG, P.C.
 STREET: Suite 1200, 127 Peachtree Street, NE
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30303-1811

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/194,981E
 FILING DATE: February 10, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Seaby
 REGISTRATION NUMBER: 38,298
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 688-0770
 TELEFAX: (404) 688-9880
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1591 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-194-981E-3

Query Match Score 17; DB 2; Length 1545;
 Best Local Similarity 100 %; Pred. No. 1.1e-02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 US-09-101-146-63
 Sequence 63, Application US/09101146
 Patent No. 6124125

GENERAL INFORMATION:
 APPLICANT: Dartmouth College, St. Vincents Institute of
 Medical Research, Kemp et al.
 TITLE OF INVENTION: NO. 6124125e1 AMP Activated Protein Kinase
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jane Massey Licata, Esq.
 STREET: 66 E. Main Street
 CITY: Marlton
 STATE: NJ
 COUNTRY: USA
 ZIP: 08053

COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 COMPUTER: IBM PC
 OPERATING SYSTEM: WINDOWS 95
 SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/101,146
 FILING DATE: October 7, 1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PNT450
 FILING DATE: 8 JAN 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane Massey Licata
 REGISTRATION NUMBER: 12,257
 REFERENCE/DOCKET NUMBER: DC-0050
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (856) 810-1515
 TELEFAX: (856) 810-1434
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1576
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 ANTI-SENSE: No
 US-09-101-146-63

Query Match Score 17; DB 3; Length 1576;
 Best Local Similarity 100 %; Pred. No. 1.1e-02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 US-08-646-273-18
 Sequence 18, Application US/08646273
 Patent No. 606502
 GENERAL INFORMATION:
 APPLICANT: Kroeger, Burkhard, Seulberger, Harald, Meyer, Thomas, Schmidt,
 Title of Invention: Endothelin Converting Enzyme (ECE).
 Number of Sequences: 36
 Correspondence Address:
 Addressee: Keil & Weinkauf
 Street: 1101 Connecticut Avenue
 City: Washington
 State: D.C.
 Country: USA
 Zip: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM AT compatible, 80486 Processor
 OPERATING SYSTEM: MS-DOS Version 6.0
 SOFTWARE: WordPerfect version 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,273
 FILING DATE: 16-NOV-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP94/03706
 FILING DATE: 11-NOV-1994
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1703 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA for mRNA
 US-08-646-273-18

Query Match 1.0%; Score 17; DB 1; Length 1852;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GGTGGGAGAAGGCCCTG 1282
 Db 1314 GTCGGGAGAAGGCCCTG 1330

RESULT 11
 US-08-238-821B-10
 ; Sequence 10, Application US/082388821B
 ; Patent No. 5912120
 ; GENERAL INFORMATION:
 ; APPLICANT: GOLDSTEIN, Joyce A.
 ; ADDRESS: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOCS/MS-DOS
 ; SOFTWARE: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
 ; TITLE OF INVENTION:
 ; TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT OF S-
 ; NUMBER OF SEQUENCES: 61
 ; TITLE OF INVENTION: MEPHYTOIN METABOLISM
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOCS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/238,821B
 ; FILING DATE: 06-MAY-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/864,962
 ; FILING DATE: 09-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Liebeschuetz, Joe
 ; REGISTRATION NUMBER: 37,505
 ; REFERENCE/DOCKET NUMBER: 15280-192110US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 326-2400
 ; TELEFAX: (650) 326-2422
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1852 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 1..10
 ; OTHER INFORMATION: /note= "Corresponds to positions 10 to 1
 ; - OTHER INFORMATION: for 65 of Figure 2."
 ; US-08-238-821B-10

Query Match 1.0%; Score 17; DB 2; Length 1852;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GGTGGGAGAAGGCCCTG 1282
 ; Sequence 10, Application US/082388821B
 ; Patent No. 5912120
 ; GENERAL INFORMATION:
 ; APPLICANT: ROMKES-SPARKS, Marjorie
 ; ADDRESS: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOCS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/201,118
 ; FILING DATE: 22-FEB-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/864,962
 ; FILING DATE: 09-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Liebeschuetz, Joe
 ; REGISTRATION NUMBER: 37,505
 ; REFERENCE/DOCKET NUMBER: 15280-192110US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 326-2400
 ; TELEFAX: (650) 326-2422
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1852 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 1..10
 ; OTHER INFORMATION: /note= "Corresponds to positions 10 to 1
 ; - OTHER INFORMATION: for 65 of Figure 2."
 ; US-08-238-821B-10

Query Match 1.0%; Score 17; DB 2; Length 1852;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1314 GTGGGGAGAACCCCTG 1330

RESULT 12 PCT-US95-05744-10
; Sequence 10, Application PC/TUS9505744GENERAL INFORMATION:
; APPLICANT: GOLDSTEIN, Joyce A.
; APPLICANT: ROMKES-SPARKS, MarjorieTITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
; CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
; NUMBER OF SEQUENCES: 61CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Khourie and CrewSTREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: CaliforniaCOUNTRY: US
ZIP: 94301COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskCOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOSSOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:APPLICATION NUMBER: US/08/201,118
FILING DATE: 22-FEB-1994CLASSIFICATION: 45
PRIORITY APPLICATION NUMBER: US 07/864,962

APPLICATION NUMBER: US 08/238,821

FILING DATE: 06-MAY-1994
PRIORITY APPLICATION NUMBER: US 08/201,118FILING DATE: 22-FEB-1994
PRIORITY APPLICATION NUMBER: US 07/864,962APPLICATION NUMBER: US 08/238,821
FILING DATE: 09-APR-1992
PRIORITY APPLICATION NUMBER: 08/201,118NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 15280-192-1-1TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1852 base pairs
; TYPE: nucleic acidSTRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: cDNA

PCT-US95-05744-10

Query Match

Best Local Similarity 100.0% ; Score 17; DB 5; Length 1852;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGAGAACCCCTG 1282

Db 1314 GTGGGGAGAACCCCTG 1330

Query Match

Best Local Similarity 100.0% ; Score 17; DB 5; Length 1852;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGAGAACCCCTG 1282

Db 1314 GTGGGGAGAACCCCTG 1330

Query Match

Best Local Similarity 100.0% ; Score 17; DB 5; Length 1852;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGAGAACCCCTG 1282

Db 1314 GTGGGGAGAACCCCTG 1330

Query Match

Best Local Similarity 100.0% ; Score 17; DB 5; Length 1852;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGAGAACCCCTG 1282

Db 1314 GTGGGGAGAACCCCTG 1330

TITLE OF INVENTION: SUBFAMILY

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/201,118

FILING DATE: 22-FEB-1994

CLASSIFICATION: 45

PRIORITY APPLICATION NUMBER:

APPLICATION NUMBER: US 07/864,962

FILING DATE: 09-APR-1992

PRIORITY APPLICATION NUMBER: 08/201,118

NAME: Liebeschuetz, Joe

REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 15280-192-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1854 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: cDNA

US - 08-201-118-4

Query Match

Best Local Similarity 100.0% ; Score 17; DB 1; Length 1854;

; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGAGAACCCCTG 1282

Db 1316 GTGTGGAGAACCCCTG 1332

Query Match

Best Local Similarity 100.0% ; Score 17; DB 1; Length 1854;

; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGAGAACCCCTG 1282

Db 1316 GTGTGGAGAACCCCTG 1332

RESULT 13 US-08-201-118-4
; Sequence 4, Application US/08201118

; Patent No. 5786191

GENERAL INFORMATION:

; APPLICANT: GOLDSTEIN, Joyce A.

; APPLICANT: ROMKES-SPARKS, Marjorie

; TITLE OF INVENTION: CLONING AND EXPRESSION OF COMPLEMENTARY

; DNAs FOR MULTIPLE MEMBERS OF THE HUMAN CYTOCHROME P450 2C

; TITLE OF INVENTION:

; STATE: California

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/238,821B

FILING DATE: 06-MAY-1994

CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/201,118
 FILING DATE: 22-FEB-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/864,962
 FILING DATE: 09-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebeschuetz, Joe
 REGISTRATION NUMBER: 37,505
 REFERENCE/DOCKET NUMBER: 15280-192110US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 326-2410
 TELEFAX: (650) 326-2422
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1854 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: Region
 LOCATION: 1..112
 OTHER INFORMATION: /note= "Corresponds to positions -12 to -1
 for 25 of Figure 2."
 US-08-238-821B-4

Query Match Score 17; DB 2; Length 1854;
 Best Local Similarity 100%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1266 GTGTGGAGAACCCCTG 1282
 Db 1316 GTGTGGAGAACCCCTG 1332

Search completed: January 7, 2003, 20:22:20
 Job time : 72.0864 secs

RESULT 15
 PCT-US95-05744-4
 Sequence 4, Application PC/TU9505744
 GENERAL INFORMATION:
 APPLICANT: GOLDSTEIN, Joyce A.
 APPLICANT: RONKES-SPARKS, Marjorie
 APPLICANT: DE MORAIS, Sonia M.F.
 TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
 CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT
 OF S-MEPHYNTOIN METABOLISM
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05744
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/238,821
 FILING DATE: 06-MAY-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/201,118
 FILING DATE: 22-FEB-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/864,962

According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:
Published_Applications_NA contains nucleic acid sequences; the search results will have the extension .rnpb.
Published_Applications_AA contains amino acid sequences; the search results will have the extension .rapb.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may request that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

Scoring table: OLIGO_NUC									
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perfect score: 1722									
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Run on: January 6, 2003, 17:17:03 ; Search time 500.308 Seconds (without alignments) 1486.844 Million cell updates/sec									
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Gapext 60.0 , Gapext 60.0									
Searched: 381593 seqs, 21652194 residues									
Word size : 15									
Total number of hits satisfying chosen parameters: 1562									
Minimum DB seq length: 0									
Maximum DB seq length: 2000000000									
Post-processing: Listing first 45 summaries									
Database : Published Applications_NA*									
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No. Score Match Length DB ID Description									
1	1722	100.0	1722	10	US-09-826-581-3	Sequence 3, Appli	Query Match	100.0%	Score 1722; DB 10; Length 1722;
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c	168	9.8	1647	10	US-09-826-581-5	Sequence 5, Appli	Matches 1722;	0;	Mismatches 0;
c	65	3.8	92	10	US-09-864-761-20146	Sequence 20146, A	Conservative	0;	Indels 0;
c	5	1.9	190	10	US-09-864-761-27246	Sequence 27246, A	0;	Gaps 0;	
c	6	1.9	1.1	229	9	US-09-826-296-2	Sequence 2, Appli		
c	7	1.9	1.1	239	9	US-09-826-296-1	Sequence 1, Appli		
c	8	1.9	1.1	389	9	US-09-032-296-5	Sequence 5, Appli		
c	9	1.9	1.1	413	9	US-09-032-296-6	Sequence 6, Appli		
c	10	1.9	1.1	422	9	US-09-939-436-362	Sequence 362, Appli		
c	11	1.9	1.1	422	9	US-09-939-298-A-362	Sequence 362, Appli		
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c	15	1.1	422	9	US-09-980-730-362	Sequence 362, Appli			
c	16	1.1	422	9	US-09-930-436-362	Sequence 362, Appli			
c	17	1.1	422	9	US-09-991-181-362	Sequence 362, Appli			
c	18	1.1	422	9	US-09-931-687-362	Sequence 362, Appli			
c	19	1.1	422	10	US-09-889-722-362	Sequence 362, Appli			

RESULT 2
US-09-864-761-3373/c
Sequence 3373, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687


```

NUMBER OF SEQ ID NOS: 49117
SOFTWARE: AnnoMax Sequence Listing Engine vers. 1.1
SEQ ID NO: 20146
LENGTH: 92
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009974.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.4
OTHER INFORMATION: NT HIT: gi|11430152, EVALUE 2.00e-22
OTHER INFORMATION: EST HUMAN HIT: BB327467.1, EVALUE 3.00e-06
OTHER INFORMATION: SWISSPROT HIT: P54619, EVALUE 3.00e-03

US-09-864-761-20146

Query Match          3.8%; Score 65; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.3e-22;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCTGGCCCTCTAGATCAAGAGCCCTCTTGCTGTGGCAACGGTGTGCCGGCAGC 60
Db      65 CCTGGCCCTCTAGATCAAGAGCCCTCTTGCTGTGGCAACGGTGTGCCGGCAGC 6

Qy      61 CCCTC 65
Db      5 CCCTC 1

RESULT 5
US-09-864-761-27246
; Sequence 27246, Application US/09864761
; Patent No. US20030048763A1
; GENERAL INFORMATION:
;   APPLICANT: Penn, Shannon G.
;   APPLICANT: Rank, David R.
;   APPLICANT: Hanzel, David K.
;   APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR MICROARRAY
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acenica-X-1
; CURRENT APPLICATION NUMBER: US/09/864 761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263 6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666

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; PRIORITY: FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00662
; PRIORITY FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00661
; PRIORITY APPLICATION NUMBER: PCT/US01/00660
; PRIORITY FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: PCT/US01/00670
; PRIORITY FILING DATE: 2001-01-30
; PRIORITY APPLICATION NUMBER: US 60/234,687
; PRIORITY FILING DATE: 2000-09-21
; PRIORITY APPLICATION NUMBER: US 09/608,408
; PRIORITY FILING DATE: 2000-06-30
; PRIORITY APPLICATION NUMBER: US 09/774,203
; PRIORITY FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annotimax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 27246
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004108.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.78
; OTHER INFORMATION: SWISSPROT HIT: P32595, EVALUATE 7.60e-01
; OTHER INFORMATION: NT HIT: E416793.2, EVALUATE 4.40e-01
; OTHER INFORMATION: EST_HUMAN HIT: BE300286.1, EVALUATE 1.70e-01
US-09-864-761-27246 LENGTH: 190

Query Match Score 19; DB 10; Length 190;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1232 CATTCTGTGAGCTGTTTG 1250
Db 90 CATTCTGTGAGCTGTTTG 108

RESULT 6
US-09-094-296-2/c
Sequence 2, Application US/09092296
Publication No. US20020188114A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: KLAAS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,296
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 60/048,810
 FILING DATE: 05-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Chery L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6104.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEX:
 INFORMATION FOR SEQ ID NO: 2 :
 SEQUENCE CHARACTERISTICS:
 LENGTH: 229 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-092-296-2

Query Match 1.1%; Score 19; DB 9; Length 229;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 116 TGAAGGGAGATGGAGGG 134
 Db 222 TGAAGGGAGATGGAGGG 204

RESULT 7 US-09-092-296-1/c
 Sequence 1, Application US/09092296
 Publication No. US20020188114A1
 GENERAL INFORMATION:
 APPLICANT: BILLING-MEDEL, PATRICIA
 APPLICANT: COHEN, MAURICE
 APPLICANT: COLDITTS, TRACEY L.
 APPLICANT: COHEN, MICHAEL R.
 APPLICANT: FRIEDMAN, PAULA N.
 APPLICANT: KLAAS, MICHAEL R.
 APPLICANT: RUSSELL, JOHN C.
 APPLICANT: STROUPE, STEPHEN D.
 TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
 FOR DETECTING DISEASES OF THE LUNG
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/092,296
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/048,810
 FILING DATE: 05-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Chery L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6104.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEX:
 INFORMATION FOR SEQ ID NO: 1 :

SEQUENCE CHARACTERISTICS:
 LENGTH: 239 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-092-296-1

Query Match 1.1%; Score 19; DB 9; Length 239;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 116 TGAAGGGAGATGGAGGG 134
 Db 226 TGAAGGGAGATGGAGGG 208

RESULT 8 US-09-092-296-5/c
 Sequence 5, Application US/09092296
 Publication No. US20020188114A1
 GENERAL INFORMATION:
 APPLICANT: BILLING-MEDEL, PATRICIA
 APPLICANT: COHEN, MAURICE
 APPLICANT: COLDITTS, TRACEY L.
 APPLICANT: COHEN, MICHAEL R.
 APPLICANT: RUSSELL, JOHN C.
 APPLICANT: STROUPE, STEPHEN D.
 TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
 FOR DETECTING DISEASES OF THE LUNG
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/092,296
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/048,810
 FILING DATE: 05-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Becker, Chery L.
 REGISTRATION NUMBER: 35,441
 REFERENCE/DOCKET NUMBER: 6104.US.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847/935-1729
 TELEX:
 INFORMATION FOR SEQ ID NO: 5 :
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-092-296-5

Query Match 1.1%; Score 19; DB 9; Length 389;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 19; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 116 TGAAGGGAGATGGAGGG 134

Db 196 TCAAGGGGATGGAGGG 178

RESULT 9
US-09-092-296-6/c
; Sequence 6, Application US/09092296
; Publication No US2002108114A1
GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COFITIS, TRACEY L.
; APPLICANT: FREIDMAN, PAULA N.
; APPLICANT: KLIASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUSE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASCSQD for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,296
; FILING DATE: 05-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,810
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6104.US.01
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 947/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
; LENGTH: 413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; US-09-092-296-6

Query Match 1.1%; Score 19; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 15; Missmatches 0; Indels 0; Gaps 0;

Qy 116 TGAGGGAGATGGAGGG 134
Db 223 TGAGGGAGATGGAGGG 205

RESULT 10
US-09-092-598-362/c
; Sequence 362, Application US/09992598
; Patent No. US201020160384A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS Encoding the Same
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIORITY NUMBER: 60/049787
; PRIORITY NUMBER: 1997-06-16
; PRIORITY NUMBER: 60/062250
; PRIORITY NUMBER: 1997-10-17
; PRIORITY NUMBER: 60/065186
; PRIORITY NUMBER: 1997-11-12
; PRIORITY NUMBER: 60/065311
; PRIORITY NUMBER: 1997-11-13
; PRIORITY NUMBER: 60/066770
; PRIORITY NUMBER: 1997-11-24
; PRIORITY NUMBER: 60/075945
; PRIORITY NUMBER: 1998-02-25
; PRIORITY NUMBER: 60/078910
; PRIORITY NUMBER: 1998-03-20
; PRIORITY NUMBER: 60/083222
; PRIORITY NUMBER: 1998-04-28
; PRIORITY NUMBER: 60/084600
; PRIORITY NUMBER: 1998-05-07
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; PRIORITY NUMBER: 1998-05-28
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; PRIORITY NUMBER: 60/087609
; PRIORITY NUMBER: 1998-06-02
; PRIORITY NUMBER: 60/087759
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; PRIORITY NUMBER: 60/088021
; PRIORITY NUMBER: 60/088025
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; PRIORITY NUMBER: 1998-06-04
; PRIORITY NUMBER: 60/088033
; PRIORITY NUMBER: 1998-06-04
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; PRIORITY NUMBER: 1998-06-04
; PRIORITY NUMBER: 60/088167
; PRIORITY NUMBER: 60/088202
; PRIORITY NUMBER: 60/088212
; PRIORITY NUMBER: 60/088212

PRIOR FILING DATE : 1998-06-05
PRIOR APPLICATION NUMBER : 60/088217
PRIOR FILING DATE : 1998-06-05
PRIOR APPLICATION NUMBER : 60/088655
PRIOR FILING DATE : 1998-06-09
PRIOR APPLICATION NUMBER : 60/088734
PRIOR FILING DATE : 1998-06-10
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PRIOR FILING DATE : 1998-06-19
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PRIOR FILING DATE : 1998-06-19
PRIOR APPLICATION NUMBER : 60/089952
PRIOR FILING DATE : 1998-06-19
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PRIOR APPLICATION NUMBER : 60/090254
PRIOR FILING DATE : 1998-06-22
PRIOR APPLICATION NUMBER : 60/090349
PRIOR FILING DATE : 1998-06-23
PRIOR APPLICATION NUMBER : 60/090355
PRIOR FILING DATE : 1998-06-23
PRIOR APPLICATION NUMBER : 60/090429
PRIOR FILING DATE : 1998-06-24
PRIOR APPLICATION NUMBER : 60/090431
PRIOR FILING DATE : 1998-06-24
PRIOR APPLICATION NUMBER : 60/090435
PRIOR FILING DATE : 1998-06-24
PRIOR APPLICATION NUMBER : 60/090444

; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Klijavrin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P7730PLIC66
 ; CURRENT APPLICATION NUMBER: US/09/989,293A
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1997-11-12
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 PRIOR APPLICATION NUMBER: 60/091544
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 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 1.1%; Score 19; DB 9; Length 422;

Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;

Qy 116 TGAAGGGAGATGAGGAGG 134
 Db 234 TGAAACGGAGATGAGGAGG 216

RESULT 12
 US-10-063-547-65/c
 Sequence 65, Application US/10063547
 GENERAL INFORMATION:
 Publication No. US20020182638A1
 APPLICANT: Bacon,Dan L.
 APPLICANT: Filvaroff,Ellen
 APPLICANT: Gerritsen,Mary E.
 APPLICANT: Goddard,Audrey
 APPLICANT: Grimaldi,Paul J.
 APPLICANT: Grimaldi,Christopher J.
 APPLICANT: Gurney,Austin L.
 APPLICANT: Watanabe,Colin K.
 APPLICANT: Wood,William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEAR ACIDS ENCODING THE SAME
 FILE REFERENCE: P3230R1C1
 CURRENT APPLICATION NUMBER: US/10/063,547
 CURRENT FILING DATE: 2002-05-02
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO: 65
 LENGTH: 422
 TYPE: DNA

i ORGANISM: Homo Sapien
 i US-10-063-547-65
 Query Match 1.1%; Score 19; DB 9; Length 422;
 Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Missmatches 0;
 Qy 116 TGAACGGAGATGAGGAGG 134
 Db 234 TGAAACGGAGATGAGGAGG 216
 RESULT 13
 US-09-989-735-362/c
 Sequence 362, Application US/09989735
 GENERAL INFORMATION:
 Publication No. US2002019299A1
 APPLICANT: Ashkenazi,Avi J.
 APPLICANT: Botstein,David
 APPLICANT: Desnoyers,Luc
 APPLICANT: Eaton,Dan L.
 APPLICANT: Ferrara,Napoleone
 APPLICANT: Fong,Sherman
 APPLICANT: Gerber,Hanspeter
 APPLICANT: Gerritsen,Mary E.
 APPLICANT: Goddard,Audrey
 APPLICANT: Godowski,Paul J.
 APPLICANT: Grimaldi,J.Christopher
 APPLICANT: Gurney,Austin L.
 APPLICANT: Kijaviv,Ivar J.
 APPLICANT: Napier,Mary A.
 APPLICANT: Par,James
 APPLICANT: Pacini,Nicholas F.
 APPLICANT: Roy,Margaret Ann
 APPLICANT: Stewart,Timothy A.
 APPLICANT: Tunas,Daniel
 APPLICANT: Watanabe,Colin K.
 APPLICANT: Williams,P. Mickey
 APPLICANT: Wood,William I.
 APPLICANT: Zhang,Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
 FILE REFERENCE: P2230P1C1
 CURRENT APPLICATION NUMBER: US/09/989,735
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
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 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
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 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR APPLICATION NUMBER: 60/087827

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; PRIOR FILING DATE: 1998-06-18          Query Match 1.1%; Score 19; DB 9; Length 422;
; PRIOR APPLICATION NUMBER: 60/089908      Best Local Similarity 100.0%; Pred. No. 15;
; PRIOR FILING DATE: 1998-06-18          Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; PRIOR APPLICATION NUMBER: 60/089947      PRIOR FILING DATE: 1998-06-19

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Qy 116 TGAAGGGAGATGGAGGAGG 134
 Db 234 TGAAGGGAGATGGAGGAGG 216

RESULT 14 - 990-444-362/C

GENERAL INFORMATION:

Publication No. US2002193300A1

APPLICANT: Ashkenazi Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavim, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730PIC19

CURRENT APPLICATION NUMBER: US/09/990,444

CURRENT FILING DATE: 2001-11-14

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Query Match          1.18;      Score 19;    DB 9;      Length 422;
Best Local Similarity 100.0%;  Pred. No. 15;      Gaps 0;
Matches 19;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Oy    116 TGAAGGGAGATGGAGGAGG 134
Db    234 TGACGGAGATGGAGGAGG 216

RESULT 15
US-09-989-730-362/C

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match Score 1.1%; DB 9; Length 422;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conserves 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 116 TGAGGGAGATGGAGGAG 134
Db 234 TGAGGGAGATGGAGGAG 216

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Search completed: January 7, 2003, 20:17:30
 Job time : 506.908 secs

GenCore version 5.1.3									
Copyright (c) 1993 - 2003 Compugen Ltd.									
1 nucleic - nucleic search, using sw model									
An on: January 6, 2003, 09:44:42 ; Search time 2203.49 Seconds (without alignments)									
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Gapov: 60.0 , Gapext: 60.0									
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Total number of hits satisfying chosen parameters:	56052								
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Maximum DB seq length: 2000000000									
Post-processing: Listing first 45 summaries									
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4	25	1.5	576	10	AW12884		AW12763 RC3-ST018		
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SUMMARIES									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
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SUMMARIES									
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SUMMARIES									
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2	38	2.2	572	13	BI34527	373008 MA	AW12866 RC3-ST018		
3	25	1.5	544	10					

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RESULT 4				REFERENCE 1 (bases 1 to 632) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.	
LOCUS	AW812884	AW812884	576 bp	mRNA linear	EST 17-MAY-2000
DEFINITION	RC3-ST0186-300100-017-h03	ST0186	Homo sapiens cDNA, mRNA sequence.		
ACCESSION	AW812884	AW812884	1	GI:7905878	EST.
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.P., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.				
COMMENT					
JOURNAL					
MEDLINE					
TITLE					
sequence tags					
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)					
COMMENT					
CONTACT:	Simpson A.J.G.				
Laboratory of Cancer Genetics					
Ludwig Institute for Cancer Research					
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil					
Tel: +55-11-2704922					
Fax: +55-11-2707001					
Email: asimpson@ludwig.org.br					
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl1=&tl2=RC3-ST0186-3000-017-h03&t3=2000-01-30&t4=1)					
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High quality sequence start:	13				
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/db_xref="taxon:9606"					
/clone lib="ST0186"					
/dev stage="adult"					
NOTE: "Organ: stomach; Vector: puc18; Site 1: Smal; Site 2: Small; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."					
BASE COUNT					
ORIGIN					
Query Match					
Best Local Similarity					
Matches 25;					
Conservative 0;					
Mismatches 0;					
Indels 0;					
Gaps 0;					
Score 25;					
DB 10;					
Length 576;					
EST 17-MAY-2000					
LOCUS	AW812763	AW812763	632 bp	mRNA linear	EST 17-MAY-2000
DEFINITION	RC3-ST0186-181099-012-h08	ST0186	Homo sapiens cDNA, mRNA sequence.		
ACCESSION	AW812763	AW812763	1	GI:7905757	EST.
VERSION					
KEYWORDS					
TITLE					
Shotgun sequencing of the human transcriptome with ORF expressed					

JOURNAL	Sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	FEATURES source	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-ST0186-181099-012-d10&t3=1999-10-18&t4=1)
MEDLINE COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br	ORGANISM	Organism: "Homo sapiens" /db_xref="TAXON:9606" /clone_lib="ST0186" /dev_stage="Adult" /not_e="Organ: stomach; Vector: puc18; Site: 1; SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
FEATURES source	BASE COUNT ORIGIN /db_xref="TAXON:9606" /clone_lib="ST0186" /dev_stage="Adult" /not_e="Organ: stomach; Vector: puc18; Site: 1; SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."	Query Match Best Local Similarity 1.5%; Score 25; DB 10; Length 661; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 8 A2293182 LOCUS A2293182 458 bp DNA linear GSS 27-JUL-2000 DEFINITION RPCI-23-159017 TU RPCI-23 Mus musculus genomic clone RPCI-23-159017 ACCESSION A2293182 VERSION A2293182.1 GI:9534967 KEYWORDS GSS. SOURCE house mouse. ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatsman,S., Akinset, AUTHORS ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Kroli,M., de Jong,P. and Fraser,C.M. TITLE Mouse BAC End Sequences From Library RPCI-23 JOURNAL Unpublished (1999) COMMENT Other GSS: RPCI-23-159017.TV Contact: Shaving Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Email: szhao@igb.org Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter.dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bcpac.med.buffalo.edu/orderingrame.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tgb/bac_ends/mouse/bac_end_intro.html Plate: 159 Row: 0 Column: 17 Seq primer: SP6 Class: BAC ends.
JOURNAL MEDLINE COMMENT	RESULT 7 AWB12746 LOCUS AWB12746 661 bp mRNA linear EST 17-MAY-2000 DEFINITION RC3-ST0186-181099-012-d10 ST0186 Homo sapiens cDNA, mRNA sequence. ACCESSION AWB12746 VERSION AWB12746.1 GI:7905740 KEYWORDS EST. SOURCE Homo sapiens ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cacorrhini; Hominidae; Homo. REFERENCE Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Ngai,M.A., da Silveira,W.Jr., Zago,M.A., Bordim,S., Costa,F.P., Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and Simpson,A.J. TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) JOURNAL MEDLINE COMMENT Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br	FEATURES source	Organism: "Mus musculus" /strain="C57BL/6J", /db_xref="TAXON:10090" /clone="RPCI-23-159017"

/clone lib="RPCI-23"				
/sex="Female"				
/lab host="DH10B"				
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BASE COUNT	142	a	74	c
ORIGIN	117	g	125	t
Query Match	1.4%	Score 24;	DB 17;	Length 458;
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Matches 24;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	109	GGGAGGTGAAGGGAGATGGAGGA	132	
Db	41	GGGAGGTGAAGGGAGATGGAGGA	64	
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LOCUS	BE126712	461 bp	mRNA	linear EST 15-JUN-2000
DEFINITION	DEPA460 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5'			
ACCESSION	BE126712			
KEYWORDS	EST.			
SOURCE	Rattus norvegicus			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
REFERENCE	Sleeman,M.A., Murison,J.G., Strachan,L., Kumble,K.D., Glenn,M.P., McGrath,A., Grierson,A., Havalkal,I., Tan,P.L.J. and Watson,J.D.			
AUTHORS				
TITLE	Expressed sequence tags of cDNA clones from rat dermal papilla cells			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Sleeman MA Biology Genesis Research and Development Corporation Limited P.O. Box 50, 1 Fox St., Parnell, Auckland, New Zealand Tel: 0064 9 373 5600 Fax: 0064 9 373 2189 Email: m.sleeman@genesis.co.nz			
	Seq primer: T3 forward High quality sequence stop: 461.			
FEATURES source	Location/Qualifiers 1..461			
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	/clone_lib="Rat Lambda ZAP Express Library"			
	/tissue_type="vibrissa"			
	/cell_type="dermal papilla"			
BASE COUNT	117	a	109	g
ORIGIN	114	c	121	t
RESULT 11				
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Qy	555	ATGCTGACCATCACAGACTTCACTGCATC	578	
Db	146	ATGCTGACCATCACAGACTTCACTGCATC	169	
RESULT 12				
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DEFINITION	pg11n.pk008.c13 Normalized Liver Library Gallus gallus cDNA clone pg11n.pk008..c13 5' similar to gii_4506061 ref[NP_002724.1] protein kinase, AMP-activated, gamma 1 non-catalytic subunit: AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens] gii_12737489 ref[XP_006778..2] protein kinase, AMP-activated, gamma 1			
Qy	555	ATGCTGACCATCACAGACTTCACTGCATC	578	
Db	246	ATGCTGACCATCACAGACTTCACTGCATC	269	
RESULT 13				
LOCUS	BM487789	595 bp	mRNA	linear EST 07-FEB-2002
DEFINITION	PGM2n-pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk005.j24 5' similar to gbaAAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus]			
ACCESSION	BM487789			
VERSION	BM487789..1			
KEYWORDS	EST.			
SOURCE	chicken			
ORGANISM	Gallus gallus			
DEFINITION	Archosauria: Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
REFERENCE	1 (bases 1 to 595)			
AUTHORS	Cogburn,L.A. and Monsonego-Ornan,E.			
TITLE	ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFFS Animal Genome Project			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1135 Fax: 302-831-2822 Email: cogburn@udel.edu, www.chickest.udel.edu.			
FEATURES source	Strains 90 & 21" /organism="Gallus gallus" /strain="Commercial broiler and Ottawa Res. Centre /clone_xref="taxon:9031" /clone_id="pgm2n..pk005..j24" /clone_lip="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)" /sex="Male and Female" /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate" /dev_stage="Breast, leg:Embryo(d19);post-hatch(1d,1,3,5,7,9,11 weeks);growth_plate(1d,7d,14d post-hatch)" /lab_host="E. coli BMDDH10B" /note="Vector: PCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"			
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Query Match	1.4%	Score 24;	DB 13;	Length 95;
Best Local Similarity	100.0%	Pred. No. 7.2;	Mismatches 0;	Indels 0;
Matches 24;	Conservative 0;			Gaps 0;
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Db	146	ATGCTGACCATCACAGACTTCACTGCATC	169	
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DEFINITION	pg11n.pk008..c13 Normalized Liver Library Gallus gallus cDNA clone pg11n.pk008..c13 5' similar to gii_4506061 ref[NP_002724.1] protein kinase, AMP-activated, gamma 1 non-catalytic subunit: AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens] gii_12737489 ref[XP_006778..2] protein kinase, AMP-activated, gamma 1			
Qy	555	ATGCTGACCATCACAGACTTCACTGCATC	578	
Db	146	ATGCTGACCATCACAGACTTCACTGCATC	169	
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LOCUS	BG713637	636 bp	mRNA	linear EST 08-MAY-2001
DEFINITION	pg11n.pk008..c13 Normalized Liver Library Gallus gallus cDNA clone pg11n.pk008..c13 5' similar to gii_4506061 ref[NP_002724.1] protein kinase, AMP-activated, gamma 1 non-catalytic subunit: AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens] gii_12737489 ref[XP_006778..2] protein kinase, AMP-activated, gamma 1			
Qy	555	ATGCTGACCATCACAGACTTCACTGCATC	578	
Db	146	ATGCTGACCATCACAGACTTCACTGCATC	169	
RESULT 16				
LOCUS	BG713637	636 bp	mRNA	linear EST 08-MAY-2001
DEFINITION	pg11n.pk008..c13 Normalized Liver Library Gallus gallus cDNA clone pg11n.pk008..c13 5' similar to gii_4506061 ref[NP_002724.1] protein kinase, AMP-activated, gamma 1 non-catalytic subunit: AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens] gii_12737489 ref[XP_006778..2] protein kinase, AMP-activated, gamma 1			
Qy	555	ATGCTGACCATCACAGACTTCACTGCATC	578	
Db	146	ATGCTGACCATCACAGACTTCACTGCATC	169	
RESULT 17				
LOCUS	BG713637	636 bp	mRNA	linear EST 08-MAY-2001
DEFINITION	pg11n.pk008..c13 Normalized Liver Library Gallus gallus cDNA clone pg11n.pk008..c13 5' similar to gii_4506061 ref[NP_002724.1] protein kinase, AMP-activated, gamma 1 non-catalytic subunit: AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens] gii_12737489 ref[XP_006778..2] protein kinase, AMP-activated, gamma 1			
Qy	555	ATGCTGACCATCACAGACTTCACTGCATC	578	
Db	146	ATGCTGACCATCACAGACTTCACTGCATC	169	
RESULT 18				
LOCUS	BM487789	595 bp	mRNA	linear EST 07-FEB-2002
DEFINITION	PGM2n-pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk005.j24 5' similar to gbaAAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus]			
ACCESSION	BM487789			
VERSION	BM487789..1			
KEYWORDS	EST.			
SOURCE	chicken			
ORGANISM	Gallus gallus			

REFERENCE		Db	305	ATGCTGACCATCACTGACTTCATC	328
AUTHORS	Burnside,J., Morgan,R.W. and Cogburn,L.A.				
TITLE	Chicken ESTs from a normalized liver library				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Joan Burnside Molecular Endocrinology University of Delaware 40 Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1345 Fax: 302-831-3411 Email: joan@udel.edu, www.chickest.udel.edu.				
FEATURES	Location/Qualifiers				
source	1..636				
/organism="Gallus gallus"					
/db_xref="taxon:9031"					
/clone="pglin_pk008_c13"					
/clone lib="Normalized Liver Library"					
/sex="Male and Female"					
/tissue_type="liver"					
/lab_host="E.coli BMH10B"					
/note="Vector: pCMVSPORT 6"					
BASE COUNT	129 a 215 c 167 g 119 t 6 others				
ORIGIN					
Query Match	1.4%	Score 24; DB 12; Length 636;			
Best Local Similarity	100.0%	Pred. No. 7.3 ; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Matches	24				
KEYWORDS					
Qy	555 ATGCTGACCATCACTGACTTCATC	578			
Db	286 ATGCTGACCATCACTGACTTCATC	309			
RESULT 12					
LOCUS	AJ451523	riken Gallus gallus	687 bp	mRNA	linear EST 22-APR-2002
DEFINITION	AJ451523	riken Gallus gallus		CDNA clone 29aari,	mRNA sequence.
VERSION	AJ451523.1				
SOURCE					
Organism:	Gallus gallus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Phasianidae; Gallinae; Aves; Neognathae; Galliformes; Phasianidae; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;					
Chicken.					
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;					
Phasianidae; Gallus.					
REFERENCE					
AUTHORS	Buerstedde,J.M.				
TITLE	Unpublished (2002)				
JOURNAL	Location/Qualifiers				
source	1..687				
/organism="Gallus gallus"					
/db_xref="taxon:9031"					
/clone="29a6rl"					
/clone lib="riken1"					
/cell_type="bursal lymphocyte"					
/dev_stage="2-3 weeks old"					
/note="CB inbred strain"					
BASE COUNT	143 a 228 c 191 g 125 t				
ORIGIN					
Query Match	1.4%	Score 24; DB 9; Length 687;			
Best Local Similarity	100.0%	Pred. No. 7.5 ; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Matches	24				
KEYWORDS					
Qy	555 ATGCTGACCATCACTGACTTCATC	578			

Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.html>) or from Research Genetics (http://www.tigr.org/tigrdb/bac_ends/mouse/bac_end_intro.html).
 Plate: 256 row: O column: 16
 Seq primer: SP6
 Class: BAC ends
 Location/Qualifiers
 1..386
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="RPCI-23-256016"
 /clone_id="RPCI-23-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACE3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electroprecipitate competent cells (BRL Life Technologies)."
 BASE COUNT 119 a 74 C 104 G 89 T
 ORIGIN

Query Match 1.3%; Score 23; DB 17; Length 386;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 110 GGGAGGTGAGGGAGATGGAGGA 132
 Db 48 GGGAGGTGAGGGAGATGGAGGA 70

RESULT 15
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 LOCUS DEFINITION 467815 MARC 2BOV Bos taurus cDNA S', mRNA sequence.
 ACCESSION BI775360
 VERSION BI775360.1
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 548)

REFERENCE AUTHORS Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J.J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keeler, J.W.
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 Genome Res. 11 (4), 626-630 (2001)
 JOURNAL
 MEDLINE
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68333-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904 e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR PRIMERS FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GTTTCGCCAGTCACGCG

Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.html>) or from Research Genetics (http://www.tigr.org/tigrdb/bac_ends/mouse/bac_end_intro.html).
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 Seq primer: ATTAGTGACATPATAG.
 Location/Qualifiers
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 /organism="Bos taurus"
 /db_xref="taxon:9013"
 /clone_id="MARC 2BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from testis, thymus,
 semitendinosus muscle, longissimus muscle, pancreas,
 adrenal, and endometrium."
 BASE COUNT 119 a 173 c 163 g 93 t
 ORIGIN

Query Match 1.3%; Score 23; DB 13; Length 548;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 CAGATCAAGAAGGGCTTCTTGC 33
 Db 487 CAGATCAAGAAGGGCTTCTTGC 509

Search completed: January 6, 2003, 11:07:53
 Job time : 22:22.49 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
 Run on: January 6, 2003, 20:16:02 ; Search time 64.9136 Seconds
 (without alignments)
 8135.386 Million cell updates/sec

Title: US-09-826-581-3
 Perfect score: 1722
 Sequence: 1 cctggccctcgatcaaga.....gatggagggtcgggctggaa 1722

Scoring table: OLIGO_NUC
 Gapop_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 15

Total number of hits satisfying chosen parameters: 989

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:
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 2: /cn2_6_ptodata/2/ina/5B_COMB.seq:
 3: /cn2_6_ptodata/2/ina/6A_COMB.seq:
 4: /cn2_6_ptodata/2/ina/6B_COMB.seq:
 5: /cn2_6_ptodata/2/ina/FCTUS_COMB.seq:
 6: /cn2_6_ptodata/2/ina/backfilesi.seq:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

989

Description

Result No.	Score	Query Match	Length	DB ID
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c 2	19	1.1	1411	1 US-08-537-942A-2
c 3	19	1.1	1411	4 US-08-997-252A-2
c 4	19	1.1	1411	4 US-09-517-739-2
c 5	19	1.1	1411	4 US-09-361-631-4
c 6	19	1.1	2993	4 US-09-361-631-3
c 7	19	1.1	40352	3 US-08-846-111D-15
c 8	18	1.1	40352	4 US-09-443-077-15
c 9	18	1.0	511	4 US-09-404-879A-68
c 10	18	1.0	740	4 US-09-312-681C-99
c 11	18	1.0	2818	4 US-0-246-489-1
c 12	18	1.0	3691	4 US-09-211-704A-3
c 13	18	1.0	3695	4 US-09-211-704A-1
c 14	18	1.0	5769	1 US-0-652-971-1
c 15	18	1.0	5769	2 US-08-699-258A-1
c 16	18	1.0	5769	2 US-08-763-399-1
c 17	18	1.0	5769	3 US-08-991-952A-1
c 18	18	1.0	9056	4 US-09-211-704A-3
c 19	18	1.0	15916	4 US-09-147-1119-5
c 20	17	1.0	495	1 US-08-215-803N-81
c 21	17	1.0	678	3 US-09-195-286-3
c 22	17	1.0	682	4 US-09-404-877A-52
c 23	17	1.0	692	4 US-09-404-877A-15
c 24	17	1.0	699	3 US-09-195-286-2
c 25	17	1.0	864	1 US-08-316-650-2
c 26	17	1.0	864	1 US-08-768-626-2
c 27	17	1.0	921	1 US-08-396-650-3

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	24	1.4	11236	1 US-07-853-913-1	Sequence 1, Appli
c 2	19	1.1	1411	1 US-08-537-942A-2	Sequence 2, Appli
c 3	19	1.1	1411	4 US-08-997-252A-2	Sequence 2, Appli
c 4	19	1.1	1411	4 US-09-517-739-2	Sequence 2, Appli
c 5	19	1.1	1411	4 US-09-361-631-4	Sequence 4, Appli
c 6	19	1.1	2993	4 US-09-361-631-3	Sequence 3, Appli
c 7	19	1.1	40352	3 US-08-846-111D-15	Sequence 15, Appli
c 8	18	1.1	40352	4 US-09-443-077-15	Sequence 15, Appli
c 9	18	1.0	511	4 US-09-404-879A-68	Sequence 68, Appli
c 10	18	1.0	740	4 US-09-312-681C-99	Sequence 99, Appli
c 11	18	1.0	2818	4 US-0-246-489-1	Sequence 1, Appli
c 12	18	1.0	3691	4 US-09-211-704A-3	Sequence 3, Appli
c 13	18	1.0	3695	4 US-09-211-704A-1	Sequence 1, Appli
c 14	18	1.0	5769	1 US-0-652-971-1	Sequence 1, Appli
c 15	18	1.0	5769	2 US-08-699-258A-1	Sequence 1, Appli
c 16	18	1.0	5769	2 US-08-763-399-1	Sequence 1, Appli
c 17	18	1.0	5769	3 US-08-991-952A-1	Sequence 1, Appli
c 18	18	1.0	9056	4 US-09-211-704A-3	Sequence 5, Appli
c 19	18	1.0	15916	4 US-09-147-1119-5	Sequence 1, Appli
c 20	17	1.0	495	1 US-08-215-803N-81	Sequence 81, Appli
c 21	17	1.0	678	3 US-09-195-286-3	Sequence 3, Appli
c 22	17	1.0	682	4 US-09-404-877A-52	Sequence 52, Appli
c 23	17	1.0	692	4 US-09-404-877A-15	Sequence 1, Appli
c 24	17	1.0	699	3 US-09-195-286-2	Sequence 2, Appli
c 25	17	1.0	864	1 US-08-316-650-2	Sequence 2, Appli
c 26	17	1.0	864	1 US-08-768-626-2	Sequence 15, Appli
c 27	17	1.0	921	1 US-08-396-650-3	Sequence 15, Appli

ALIGNMENTS

RESULT 1
 US-07-853-913-1/c
 ; Sequence 1, Application US-07053913
 ; Patent No. 538839

; GENERAL INFORMATION:

; APPLICANT: McKay, Ronald D.G.
 ; APPLICANT: Lendahl, Urban
 ; TITLE OF INVENTION: Nestin Expression As An Indicator of Neuroepithelial Tumors
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02173

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/853, 913
 ; FILING DATE: 1992-03-19
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/660, 412
 ; FILING DATE: 22-FEB-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/603, 803
 ; FILING DATE: 25-OCT-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/201, 762
 ; FILING DATE: 02-JUN-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/180, 548
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32, 227
 ; REFERENCE/DOCKET NUMBER: MIT-4641AAA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-861-5240
 ; TELEFAX: 617-861-9540
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11236 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; Sequence 3, Appli

MOLECULE TYPE: DNA (genomic)
US-07-853-913-1

RESULT 2
US-08-537-942A-2
Sequence 2, Application US/08537942A
Patent No. 5153464
GENERAL INFORMATION:
APPLICANT: HIRANO, TOSHIO
APPLICANT: KISHIO, NISHINOMIYA
TITLE OF INVENTION: PROTEIN ENCODING A POLYPEPTIDE HAVING A
TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPLIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,942A
FILING DATE: 21-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00819
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-141178
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4767-004-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-4220
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: sig peptide
LOCATION: 1..84
OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
US-08-537-942A-2
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1613 ACAGCACCCATCTGACTG 1631
Db 948 ACAGCACCCATCTGACTG 966

TITLE OF INVENTION: GENE ENCODING A POLYPEPTIDE HAVING A
 TITLE OF INVENTION: PRE-B CELL GROWTH-SUPPORTING ABILITY
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIERS & NEUSTADT,
 ADDRESS: P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/517,739
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/997,252
 FILING DATE: 23-DEC-1997
 APPLICATION NUMBER: US 08/537,942
 FILING DATE: 21-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP94/00819
 FILING DATE: 20-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 5-141178
 FILING DATE: 21-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 4767-0005-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-412-2220
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1411 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 FEATURE:
 NAME/KEY: sig peptide
 LOCATION: 1..84
 OTHER INFORMATION: /note= "IDENTIFICATION METHOD: E"
 US-09-517-739-2

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 Matches 19; Conservative 0; Mismatches 0; Indels 0

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Db	948	ACAGCACCATTCTGACTG	966

RESULT 5
 US-09-361-631-4/C
 Sequence 4, Application US/09361631
 ; Patent No. 638778
 ; GENERAL INFORMATION:
 ; APPLICANT: Zuker, Charles S.
 ; APPLICANT: Adler, Jon Elliot
 ; APPLICANT: Lindemeyer, Juergen
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
 ; TITLE OF INVENTION: Involved in Sensory Transduction
 ; CURRENT APPLICATION NUMBER: US/09/361-631
 FILE REFERENCE: P-03200-08872015

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CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2532
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: mouse G-protein coupled receptor sequence
US-09-361-631-4

Query Match Score 1.1%; Best Local Similarity 100.0%; Pred. No. Matches 19; Conservative 0; Mismatch 1
Qy 119 AGGGAGATGGAGGGGTGA 137
Db 2339 AGGGAGATGGAGGGGTGA 2321

RESULT 6
US-09-361-631-3/c
; Sequence 3, Application US/09361631
; Patent No. 6383778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Lindemeyer Juergen
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Involved in Sensory Transduction
; FILE REFERENCE: 02304-E-007270US
; CURRENT APPLICATION NUMBER: US/09/361,631
; CURRENT FILING DATE: 1999-07-27
; EARLIER APPLICATION NUMBER: US 60/095,464
; EARLIER FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: US 60/112,747
; EARLIER FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2993
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat G-protein coupled receptor sequence
US-09-361-631-3

Query Match Score 1.1%; Best Local Similarity 100.0%; Pred. No. Matches 19; Conservative 0; Mismatch 1
Qy 119 AGGGAGATGGAGGGGTGA 137
Db 2351 AGGGAGATGGAGGGGTGA 2333

RESULT 7
US-08-846-111D-15/c
; Sequence 15, Application US/08846111D
; Patent No. 6017705
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Thierry
; APPLICANT: Boon-Faillieu, Isabelle
; TITLE OF INVENTION: Isolated Nucleic Acid
; NUMBER OF INVENTIONS: 16
; MEMBERS OF THE MAGe
```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felie & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 ZIP: 10022-7513

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect For DOS 6.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/846,111D
 FILING DATE: 25-APRIL-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/403,388
 FILING DATE: 5-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/403,388
 FILING DATE: 14-MARCH-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6017705man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5444.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-2200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40352 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-846-111D-15

Query Match 1.1%; Score 19; DB 3; Length 40352;
 Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;

US-09-443-077-15:

Query Match 1.1%; Score 19; DB 4; Length 40352;
 Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;

US-09-443-077-15:

Query Match 1.1%; Score 19; DB 4; Length 40352;
 Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;

US-09-443-077-15:

RESULT 9
 US-09-404-879A-68
 ; Sequence 68, Application US/09404879A
 ; Patent No. 6468346
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Algate, Paul A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.462C2
 ; CURRENT APPLICATION NUMBER: US/09/404,879A
 ; CURRENT FILING DATE: 1999-09-24
 ; NUMBER OF SEQ ID NOS: 393
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 68
 ; LENGTH: 511
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-404-879A-68

Query Match 1.0%; Score 18; DB 4; Length 511;
 Best Local Similarity 100.0%; Pred. No. 45; Mismatches 0; Indels 0; Gaps 0;

US-09-404-879A-68

Query Match 1.0%; Score 18; DB 4; Length 511;
 Best Local Similarity 100.0%; Pred. No. 45; Mismatches 0; Indels 0; Gaps 0;

US-09-404-879A-68

RESULT 10
 US-09-342-681C-99
 ; Sequence 99, Application US/09342681C
 ; Patent No. 6355782
 ; GENERAL INFORMATION:
 ; APPLICANT: Zonana et al.
 ; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
 ; FILE REFERENCE: 52978
 ; CURRENT APPLICATION NUMBER: US/09/342,681C
 ; CURRENT FILING DATE: 1999-06-29
 ; PRIORITY APPLICATION NUMBER: 60/092,279
 ; PRIORITY FILING DATE: 1998-07-09
 ; PRIORITY APPLICATION NUMBER: 60/112,366
 ; PRIORITY FILING DATE: 1998-12-15
 ; NUMBER OF SEQ ID NOS: 123
 ; SOFTWARE: PatentIn Ver. 2.1

RESULT 8
 US-09-443-077-15/C
 ; Sequence 15, Application US/09443077
 ; Patent No. 6392016
 ; GENERAL INFORMATION:
 ; APPLICANT: Lurquin, Christophe; Brisseau, Francis;
 ; Boon-Falleur, Thierry
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
 ; Members Of The Mage-B Family And Uses Thereof
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Felie & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; ZIP: 10022-7513
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect For DOS 6.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/443,077
 FILING DATE: 26-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/846,111
 FILING DATE: <Unknown>

SEQ ID NO 99
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-661-C-99

Query Match 1.0%; Score 18; DB 4; Length 740;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 669 CCTCCCTGAGCTGGTGC 686
Db 14 CCTCCCTGAGCTGGTGC 31

RESULT 11
US-08-246-489-1/C
; Sequence 1, Application US/08246489
; Patent No. 6225049
GENERAL INFORMATION:
; APPLICANT: Lan, Michael S.
; APPLICANT: No. 6225049kans, Abner L.
TITLE OF INVENTION: NOVEL HUMAN INSULINOMA-ASSOCIATED cDNA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: California
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,489
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/901,715
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned A.
REGISTRATION NUMBER: 29,655
REGISTRATION NUMBER: NIH012.012A
REFERENCE/DOCKET NUMBER: NIH012.012A
TELEPHONE: (619) 235-0550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2838 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: IA-1

US - 08 - 246 - 489 - 1

Query Match 1.0%; Score 18; DB 4; Length 2838;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 TGGAGGGTGGGGGG 484
Db 2544 TGGAGGGTGGGGGG 2527

RESULT 12

US-09-211-704A-3/C
; Sequence 3, Application US/09211704A
; Patent No. 627104

GENERAL INFORMATION:
; APPLICANT: de Saint-Vis, Blandine Marie
; APPLICANT: Fossiez, Francois
; APPLICANT: Caux, Christophe
; APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,704A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/005,263
FILING DATE: 09-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Chang, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: SF0781K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 343...2028
FEATURE:
NAME/KEY: mat_Peptide
LOCATION: 406...2028
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3454
OTHER INFORMATION: /note= "nucleotide 3454 designated W,
; OTHER INFORMATION: may be A or T."
US-09-211-704A-3

Query Match 1.0%; Score 18; DB 4; Length 3691;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 530 TCTCCCCGCCCTCCCC 547
Db 2389 TCTCCCCGCCCTCCCC 2372

RESULT 13

US-09-211-704A-1/C
; Sequence 1, Application US/09211704A
; Patent No. 627104

GENERAL INFORMATION:
; APPLICANT: de Saint-Vis, Blandine Marie
; APPLICANT: Fossiez, Francois

APPLICANT: Caux, Christophe
 APPLICANT: Lebecque, Serge J. E.
 TITLE OF INVENTION: Mammalian Proteinases; Related Reagents
 NUMBER OF INVENTION: and Methods
 CORRESPONDENCE ADDRESS:
 STREET: DNAX Research Institute
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94104-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0. Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/211,704A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/005,293
 FILING DATE: 09-JAN-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: SF0781K
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 852-9196
 TELEFAX: (650) 496-1200
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3695 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 344..2032
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 398..2032
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 3458
 OTHER INFORMATION: /note= "nucleotide 3458 designated
 US-09-211-704A-1
 Query Match 1.0%; Score 18; DB 4; Length 3695;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 530 TCCGCCCCCCCCCCCC 547
 Db 2393 TCCCTCCcccCcCcCCCCC 2376

RESULT 14
 US-08-652-971-1
 Sequence 1, Application US/08652971
 Patent No. 5814507
 GENERAL INFORMATION:
 APPLICANT: Cheng, Jill
 APPLICANT: Lasky, Laurence A.
 TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd.

CITY: South San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0. Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/652,971
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Deger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1033
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 235-3216
 TELEFAX: (415) 952-9881
 TELEX: 910 371 7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5769 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 379..4686
 US-08-652-971-1
 Query Match 1.0%; Score 18; DB 1; Length 5769;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 274 CTCAATTTCGGCATCTGT 291
 Db 5612 CTCAATTCCCATCTGT 5629

RESULT 15
 US-08-991-258A-1
 Sequence 1, Application US/08991258A
 Patent No. 592887
 GENERAL INFORMATION:
 APPLICANT: Cheng, Jill
 APPLICANT: Lasky, Laurence A.
 TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESS: FLEHR, HOHBACH, TEST, ALBRITON & HERBERT, LLP
 STREET: 4 Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0. Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/991,258A
 FILING DATE: 17-DEC-1997
 CLASSIFICATION: 415
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/652,971
 FILING DATE: 2-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Deger, Walter H.

REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5769 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 379..4686
US-08-991-258A-1

Query Match 1.0%; Score 18; DB 2; Length 5769;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 CTCATTCCCATCTGT 291
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Db 5612 CTCATTCCCATCTGT 5629

Search completed: January 7, 2003, 20:22:10
Job time : 207.914 secs

GenCore version 5.1.3
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model		Results						
Run on:	January 6, 2003, 16:44:13 ; Search time 4127.03 Seconds (without alignments) 1164.233 Million cell updates/sec	Result No.	Score	Query Match Length	DB ID	Description		
Title:	US-09-826-581-5	1	1647	100.0	1647	AX281582 Sequence		
Perfect score:	1647	2	1372	83.3	2115	AK099802 Sequence		
Sequence:	1 ttgtcttgggctggccaca.....acaccaggcctttatgtcttc 1647	3	1376	83.3	2109	AF214519 Homo sapi		
Scoring table:	OLIGO_NUC	4	1366	82.9	2109	AJ099776 Sequence		
Gapop:	60.0 , Gapext 60.0	5	1332	80.9	2290	AU249977 Homo sapi		
Searched:	2054640 seqs, 14551402878 residues	6	406	24.7	989	AX281579 Sequence		
Word size :	15	7	285	17.3	206854	AC009974 Homo sapi		
Total number of hits satisfying chosen parameters:	52453	8	278	16.9	1014	AX281581 Sequence		
Minimum DB seq length: 0		9	278	16.9	152129	AC027416 Homo sapi		
Maximum DB seq length: 20000000000		10	197	12.0	152129	AC027416 Homo sapi		
Post-processing: Listing first 45 summaries		11	168	10.2	1722	AX281580 Sequence		
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	gb_vl:*	24	32	1.9	227724	AF336381 Mus muscu		
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	gb_**:	27	29	1.8	192968	AC127107 Rattus no		
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	gb_vl:*	36	21	1.3	24055	Z75743 Human DNA		
	em_ba:*	37	21	1.3	52780	AC026762 Homo sapi		
	em_fun:*	38	21	1.3	66341	AC118678 Mus muscu		
	em_hum:*	39	21	1.3	67674	AC101032 Mus muscu		
	em_in:*	40	21	1.3	78184	AC067722 Homo sapi		
	em_mu:*	41	21	1.3	79414	AC023502 Homo sapi		
	em_cm:*	42	21	1.3	117362	AC094277 Rattus no		
	em_or:*	43	21	1.3	123085	AL157406 Human DNA		
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SIMONE

APPENDIX

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/protein_id="CAD10589_1"		
/translation="MEPGLPHALRRTPSWSSLGSESHOEMSPEFOENSSWSPAVTS SERTRCKRKAKLWRWDCPISDCTASASCSSTDDELECELLERPLA LSPOAEPKULWDDELRKPAQIYMRMEOHTCUDAMANSKLVIFDMLEIKAPFA LVANGYRAAPLWDSKSKQSFYQMLITDFILVHRYRSPFLQYIEBOKHETWREIY LQGCFPKLVSISPNDSLFEAVYTLIKNTHRLPVLDPVEGNVHLTHKLKFPLHIF GSLLPRPSFLYRTIDOLGICTFERDLAVVLETAPILTALEDFIVDRRVSALPVNECGQV VGLYERFEDVHILAQOTYHNLDMSVGEALROPTULEGVLSCOPHESLGEVIDRIARE		
BASE COUNT	346 a 502 c 462 g 337 t	
ORIGIN		
Query Match	100.0%	Score 1647; DB 6; Length 1647;
Best Local Similarity	100.0%	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db 1	TGGTCTGGCTGGCACATGGAGCCGGCTGGAGCAGGACTGGCAGGCCCTTC	60
Qy 61	CTGGACAGGCTGGGGTCTGAGCATCAGAGATGAGTTCTAGAGAAACAG	120
Db 61	CTGGACAGGCTGGGGTCTGAGCATCAGAGATGAGTTCTAGAGAAACAG	120
Qy 121	CAGCTATGGCATCACCAGGTGACCGAGCTGAGAAATCGTGGAAACGGAG	180
Db 121	CAGCTATGGCATCACCAGGTGACCGAGCTGAGAAATCGTGGAAACGGAG	180
Qy 181	GGCAAAGGCCTTGATGGAGAAGGTGGAGGAAGCTGGACCAAGGCTCA	240
Db 181	GGCAAAGGCCTTGATGGAGAAGGTGGAGGAAGCTGGACCAAGGCTCA	240
Qy 241	GGGGAAAGGTCCCGTCCAGGCTGGAGTCTGGAGGCTGGACCACTTCCC	300
Db 241	GGGGAAAGGTCCCGTCCAGGCTGGAGTCTGGAGGCTGGACCACTTCCC	300
Qy 301	CAAGACCAACCTTGGCTAACGTGATCTGGCTGGAGGCTAACACAGGTG	360
Db 301	CAAGACCAACCTTGGCTAACGTGATCTGGCTGGAGGCTAACACAGGTG	360
Qy 361	GGACTGCCACGGATTCCACGCCAGGGCTGGAGTCTGGAGGCTGGAGA	420
Db 361	GGACTGCCACGGATTCCACGCCAGGGCTGGAGTCTGGAGGCTGGAGA	420
Qy 421	GCTGGCCACGGATTCCACGCCAGGGCTGGAGTCTGGAGGCTGGAGA	480
Db 421	GCTGGCCACGGATTCCACGCCAGGGCTGGAGTCTGGAGGCTGGAGA	480
Qy 481	AGAGAGGCTGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540
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Qy 541	CGAACTCGGAAACCGGCCACAGATCACAGCTGAGGACACCTGCTA	600
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Qy 601	CGATGCCATGCCAACTAGCTCCACGCTAGCTCCATGCCATGCCATG	660
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RESULT 2		
Axon9802		
LOCUS	AX09802	2115 bp
DEFINITION	Sequence 29 from Patent WO0120003.	
ACCESSION	AX09802	
VERSION	AX09802.1	GI:13538836
KEYWORDS		

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
1 (bases 1 to 2115)	
Milan,D., Jeon,J.T., Loofit,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Geilin,J., Kalm,E., Roy,P.L., Chardon,P. and Anderson,J., A mutation in PRKAG3 associated with excess glycogen content in pig skeletal muscle Science 288 (54469), 1248-1251 (2000)	
JOURNAL MEDLINE PUBMED	208018001
REFERENCE AUTHORS	Milan,D.; Jeon,J.T.; Loofit,C.; Amarger,V.; Robic,A.; Thelander,M.; Rogel-Gaillard,C.; Paul,S.; Iannuccelli,N.; Rask,L.; Ronne,H.; Kalm,E.; Le Roy,P.; Chardon,P. and Anderson,L.
TITLE JOURNAL	Direct Submission Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24, Sweden
FEATURES SOURCE	Location/Qualifiers 1 . 2115 /organism="Homo sapiens" /db_xref="taxon: 9606" /chromosome="2" /map="2P" /tissue type="skeletal muscle" 1 . 2115 /gene="PRKAG3" /note="PRKAG3" /note="AMPK3" /codon_start=1 /product="AMP-activated protein kinase gamma subunit" /protein_id="AAF73987_1" /ab_xref="GI:8215682" /translation="MSFEQENSSSSWSPNATSSSERKGRKRAKALWTRQSKVEEGEPICQEGERPSRPTAESTGLEATPKTIPLAQDPAQGTPPTGWDCLPSDCTASAAGSSTDQVELATEPATANEVCELEGLWRERPAICLSPQAPPPLKGWDDDELRKPGQIYMRPFOHQHTCYDAMATSKKLVIDPDMLEIKKAFLVANGTRAILWDSSKKQSFVGMLTITDFFLVLLRYRSPLVQYIEORKHETWREYLQGCPKPLVYIISPNDSLFEAVYTLIKNTHRLPVLPDVPSGNVHLTHTRKLHLIFSLIPLRPSFLYRTIOLGLGTFRDLAVNLETAPALDIEFURRQHILVHRRQHILVHQAQOTHILDMSVGEALRQRTULCLEGVLSCOPESLUGEVIDIRAREQVHRLVLDTHQLLGVVLSLDLQALVLSPIAGIDALGA"
BASE COUNT ORIGIN	460 a 622 c 562 g 471 t
Query Match Score 83 . 3%; Best Local Similarity 99 . 9%; Pred. No. 0; Matches 1422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy 95 ATGGCTTCAGGCAAGAAAACAGCAGTCATGCCATCACCAAGCTGTGACAGCAGC 154 Dbb 1 ATGAGCTTCAGGCAAGAAAACAGCAGTCATGCCATCACCAAGCTGTGACAGCAGC 60	
Qy 155 TCGAGAAAGATTCCTGGGAAAGAACGGAGGGCCAAGAACGCTTGAGATGGACAGCAAGTGC 214 Dbb 61 TCGAAAGATCCGGAAACGGGCAACTGGGAACTGGGCAACTGGTCAAGGAGAGTGC 120	
Qy 215 TCGACGGCTGGAGCCCATTCAGGCAAGAACCAACCCCTGGCTGACGTCTGC 334 Dbb 181 TCAACGGCTGGAGCCCATTCAGGCAAGAACCAACCCCTGGCTGACGTCTGC 240	
Qy 335 GGCGTGGGCACTCCACCAACAGGGTGGGACTGCTGCCCTCTGACTGTACGGCTCAGT 394 Dbb 121 TCGAGGAAGGGCACTGGGCAACTGGGCAACTGGTCAAGGAGAGTGC 180	
Qy 241 GGCGTGGGCACTCCACCAACAGGGTGGGACTGCTGCCCTCTGACTGTACGGCTCAGT 300 Dbb 395 GCAGGCTCGAGCAAGATGAGCTGGAGTTCCAGGCCAGGGATTCCAGGCCCTG 454	
Qy 301 GCAGGGCTCAGCACAGATGGAGCTGGGACTGGCCAGGGTGGCTCCAGGCCACAGGGCTGG 360 Dbb	
Qy 455 GAGTGTGAGCTGAGAAGCTGGCTGCTGGAGAGGGCTGCCCCTGCTGCTGCCCTGCC 514 Dbb	
Qy 361 GAGTGTGAGCTGAGTGGCTGAGCTGGAGAGGGCTGCCCCTGCTGCTGCCCTGCC 420	
Qy 515 CCATTTCAGCTGGCTGGGATGAGCAACTGCGGAAACCCGGGCCACAGATCTACATG 574 Dbb	
Qy 421 CCATTTCAGCTGGCTGGGATGAGCAACTGCGGAAACCCGGGCCACAGATCTACATG 480	
Qy 575 CGCTTCATGGGGGACACCTGCTGAGCTGGCTGAGCTAGTCTCAAGCTAGTCATC 634 Dbb	
Qy 481 CGCTTCATGGGGGACACCTGCTGAGCTGGCTGAGCTAGTCTCAAGCTAGTCATC 540	
Qy 635 TTGAGACACATGCTGGAGATCAAGAGGCTTCCTTGGCTGGGATGCTGGTGGGG 694 Dbb	
Qy 541 TTGAGACACATGCTGGAGATCAAGAGGCTTCCTTGGCTGGGATGCTGGTGGGG 600	
Qy 695 GGAGGCCCTCTATGGACAGCAAGAGCAGCTTGTGGGATGCTGGTGGGG 814 Dbb	
Qy 601 GGAGGCCCTCTATGGACAGCAAGAGCAGCTTGTGGGATGCTGGTGGGG 660	
Qy 755 TTCACTCTCTGCTGCTGATGGCTGATGGCTGATGGCTGAGCTGGATGGATGGAA 720 Dbb	
Qy 661 TTCACTCTCTGCTGCTGATGGCTGATGGCTGAGCTGGATGGATGGATGGAA 720	
Qy 815 CAACATAAGATTGAGCTGGAGCTGGAGGATCTACCTGCAAGCTGCTGCTGCTG 874 Dbb	
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Qy 875 TCCATCTCTCTTAATGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 934 Dbb	
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Qy 961 CGCACTATCCAAGATTGGGCATCGCACATTCCGAGACTTGGCTGCTGGAGACA 1020	
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REFERENCE		AUTHORS	Andersson, L., Loofit, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gelin, J., le Roy, P., and Chardon, P.	TITLE	Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof	JOURNAL	PATENT NO 0120003-A 3 -22-MAR-2001	INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR) ; Andersson, Leif (SE) ; Loofit, Christian (DE) ; Kalm, Ernst (DE)	FEATURES	Location/Qualifiers	source	1..2109	/organism="Homo sapiens"	Qy	881	TCTCCTATGATAAGCCCTTGTAGCGCTTTGAGGCTTCACATGGATTCACTGC	Db	421 CCCAGCTGGCTGGATGACGAACTGGCAAACCGGCCAGATCTACATGCC
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Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong (htcp://bacpac.med.buffalo.edu).

VECTOR : PBACE.6
 NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-6705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists between 38812-38903. An unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES
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 Best Local Similarity 17.3%; Score 285; DB 9; Length 206854;
 Matches 405; Conservative 99.8%; Pred. No. 1.6e-140; Mismatches 0; Indels 1; Gaps 1;

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 Db 168466 AGGTCCCCGGTCAAGCTGACTGTCACGGGCTGAGTCACGCCACATCCCCAACAGC 168407

QY 307 CACACCCCTGGCTCAAGCTGACTGTCACGGCTCCAGCATGATGTCAGCTGCGACTCCACAAAGGCTGGACTG 366
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QY 367 CCTCCCTCTGACTGTCACGGCTCCAGCATGATGTCAGCTGCGACTCCACAAAGGCTGGACTG 426
 Db 168346 CCTCCCTCTGACTGTCACGGGCTGAGTCACGCCACATCCCCAACAGC 168287

QY 427 CACGGAGTTCCAGCCACGGCTGGAGTGAGTCAGCTGAGTCAGATGTCAGCTGCTGGAGAGAG 486
 Db 168286 CACGGAGTTCCAGCCACGGCTGGAGTGAGTCAGCTGAGTCAGATGTCAGCTGCTGGAGAG 168227

Qy	487	GCCGCCCTGTGCCCTCCCCAGGCCATTCCAAAGCTGGCTGGATGACGAAC	546		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Db	168226	GCCTGCCCTGGCGCTGTGCCCTGGCGCTTCAGCTGGATGACGAAC	168168		1 (bases 1 to 152129)
		-CCCCATTCCCAAGCTGGCGCTTCAGCTGGATGACGAAC		Birren, B., Linton, L., Nusbaum, C., Lander, E., and Lander, E.	
				Unpublished	
Qy	547	GGCAAACCCGGCCGAGATCTACATGCCCTCATGCCAGAGCACCTGCTGGATGACGAAC	606		2 (bases 1 to 152129)
Db	168167	GGCAAACCCGGCCGAGATCTACATGCCCTCATGCCAGAGCACCTGCTGGATGACGAAC	168108		Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhalter, B., Brown, A., Burlett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelio, M., Collins, S., Collymore, A., Cooke, P., DeReuelano, K., Diaz, J. S., Dodge, S., Donino, M., Doyle, M., Ferrira, P., FitzHugh, W., Gage, D., Galagan, J., Gardna, S., Ginde, S., Govertse, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LeRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, J., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEvany, P., McDurk, A., McKernan, K., McPheeters, R., Melidrin, J., Menes, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M., Oliver, J., Peterkin, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassilev, H., Vidal, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainour, J., Zimmer, A., and Zody, M.
Qy	607	CATGGCAACTCTCAGCTTCTGACTCTTGACACCATGCTGGAG	652		Direct Submission
Db	168107	CATGGCAACTCTCAGCTTCTGACTCTTGACACCATGCTGGAG	168062		Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
				On Jun 7, 2000 this sequence version replaced gi:7342115.	
				All repeats were identified using RepeatMasker:	
				Smit, A.F.A. & Green, P. (1996-1997)	
				http://ftp.genome.washington.edu/Rn/RepeatMasker.html	
				----- Genome Center	
				Center: Whitehead Institute/ MIT Center for Genome Research	
				Center code: WIBR	
				Web site: http://www-seq.wi.mit.edu	
				Contact: sequence_submissions@genome.wi.mit.edu	
				----- project information	
				Center project name: L7458	
				Center clone name: 504_C11	
				----- Summary Statistics	
				Sequencing vector: M13: M77815; 100% of reads	
				Chemistry: Dye-terminator Big Dye; 100% of reads	
				Abase program: Phrap; version: 0.960731	
				Consensus quality: 135376 bases at least Q40	
				Consensus quality: 143264 bases at least Q30	
				Consensus quality: 146503 bases at least Q20	
				Insert size: 161000; agarose-IP	
				Insert size: 149029; sum-of-contigs	
				Quality coverage: 3.1 in Q20 bases; agarose-IP	
				Quality coverage: 3.3 in Q20 bases; sum-of-contigs	

				* NOTE: This is 'working draft' sequence. It currently	
				* consists of 32 contigs. The true order of the pieces	
				* is not known and their order in this sequence record is	
				* arbitrary. Gaps between the contigs are represented as	
				* runs of N, but the exact sizes of the gaps are unknown.	
				* This record will be updated with the finished sequence	
				* as soon as it is available and the accession number will	
				* be preserved.	
				* 1 1006 1105: gap of 1005 bp in length	
				* 1 1106 12402: contig of 1297 bp in length	
				* 2403 2502: 369 bp of 100 bp	
				* 2503 3823: contig of 1321 bp in length	
				* 3824 3933: 949 bp of 100 bp	
				* 3924 5020: contig of 1097 bp in length	
				* 5021 5120: 549 bp of 100 bp	
				* 5121 6161: contig of 1041 bp in length	
				* 6162 6261: 949 bp of 100 bp	
				* 6262 7547: contig of 1286 bp in length	
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LOCUS					
DEFINITION		AC027416 15129 bp DNA linear HTG_07-JUN-2000			
ACCESSION		Homo sapiens clone RP1-504G11, WORKING DRAFT SEQUENCE, 32 unorderd pieces.			
VERSION		AC027416..2 GI:8317289			
KEYWORDS		HTGS PHASE1 HTGS_DRAFT			
SOURCE		Homo sapiens			
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

LOCUS AC027416 152129 bp DNA linear HTG 07-JUN-2000
 DEFINITION Homo sapiens clone RP11-504G11, WORKING DRAFT SEQUENCE, 32
 UNORDERED pieces.

ACCESSION AC027416
 VERSION 2 GI:8317289
 KEYWORDS HTGS_PHASE1; HTGS_DRAFT.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 152129)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens, clone RP11-504G11
 Unpublished

2 (bases 1 to 152129)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abramam, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
 Boguslavskiy, L., Boukigaalter, B., Brown, A., Burkett, G.,
 Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S.,
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 Howland, J., Iliev, I., Johnson, R., Jones, C., Kann, J., Karatas, A.,
 Klein, J., LaRocque, K., Lanzarotti, R., Landers, T., Lehozky, J.,
 Levine, R., Lieu, C., Liu, G., Locke, K., McDonald, P., Marquis, N.,
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
 Meldrim, J., Menets, J., Minova, T., Miranda, C., Mienga, V., Morrow, J.,
 Murphy, T., Naylor, J. M., Norman, C. H., O'Connor, T., O'Donnell, P.,
 O'Neil, D., Oliver, T., Peterson, K., Pierre, N.,
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Teafay, C. S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
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 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

JOURNAL

REFERENCE AUTHORS TITLE

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abramam, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
 Boguslavskiy, L., Boukigaalter, B., Brown, A., Burkett, G.,
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 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

JOURNAL

COMMENT Submitted (10-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 7, 2000 this sequence version replaced gi:7342115.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

JOURNAL

COMMENT Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L7458
 Center clone name: 504 G.11
 ----- Summary Statistics
 Sequencing vector: M13; M7815; 100% of reads
 Chemistry: dye-terminator
 Assembly program: Phrap; version 0.960731
 Consensus quality: 1153376 bases at least Q40
 Consensus quality: 143264 bases at least Q30
 Consensus quality: 146503 bases at least Q20
 Insert size: 161000; agarose-ip
 Insert size: 143029; sum-of-contigs
 Quality coverage: 3.1 in Q20 bases; agarose-fp
 Quality coverage: 3.3 in Q20 bases; sum-of-contigs

FEATURES source
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 32 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1005: contig of 1005 bp in length
 * 1006 1105: gap of 100 bp

Location Qualifiers
 1. 152129

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 Db 38059 AGTGTGAGCTAGAAGGCCATGCTGGAGAGCCACTGGAACTGCAAGGTAGTCATCT
 Qy 516 CATTTCCTCAAAGCTGGCTGGAGAACCGGGGCCAGATCTACATGC 575
 Db 38119 CATTTCCTCAAAGCTGGCTGGAGAACCGGGGCCAGATCTACATGC 38060
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Db 37999 TCGACACCAGTGCTGGAG 37983

RESULT 11 AX281580 LOCUS AX281580 Sequence 3 from Patent WO0177305. DNA linear PAT 03-NOV-2001
 DEFINITION AX281580
 ACCESSION AX281580
 VERSION AX281580.1 GI:16608831
 KEYWORDS human,
 SOURCE human,
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Andersson,L., Luthman,H. and Marklund,S.
 TITLE Variants of the human amp-activated protein kinase gamma 3 subunit
 JOURNAL Patent: WO 0177305 A 3 18-OCT-2001;
 Arxix AB (SE)
 FEATURES Location/Qualifiers
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 ORIGIN 0;

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RESULT 12 G67375 LOCUS G67375 Human Homo sapiens STS genomic, sequence tagged site.
 DEFINITION G67375
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 VERSION G67375.1
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 106)
 AUTHORS Robic,A., Jeon,J.-T., Rey,V., Amarger,V., Chardon,P., Loots,C.,
 Anderson,L., Geilin,J. and Milan,D.
 TITLE Construction of a high-resolution RH map of human 2q35 region on
 TNG panel and comparison with physical map of porcine homologous
 region 15q25
 JOURNAL COMMENT Unpublished (2001)

Contact: Annie ROBIC, Denis MILAN
 Genetique Cellulaire
 Institut National de Recherche agronomique (INRA)
 Bp227, 31326 Castanet Tolosan, France
 Tel: (33) 5 61 28 51 21
 Fax: (33) 5 61 28 53 08
 Email: arobic@toulouse.inra.fr
 Primer A: TGGGCATCGGCCACATTC
 Primer B: GACACAGGAGTGGAGA
 PCR Profile:
 Initial incubation: 94 degrees C 5 min

Denaturation: 94 degrees C for 30 seconds
 Annealing: 55 degrees C for 30 seconds
 Polymerization: 72 degrees C for 30 seconds
 Thermal cycler: Perkin Elmer 9600
 Protocol:
 Template: 25 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.1 units/reaction
 Total Vol: 15 uL

Buffer:

MgCl₂: 2 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.4

Primers were defined on sequence AA178898 (cDNA). No intron.

FEATURES	Location/Qualifiers	Source	DEFINITION	SEQUENCE
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	/clone_lib="Human"		KEYWORDS pig, Sus scrofa	
	1..>106		ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Bokaryota; Metazoa; Cetartiodactyla; Suiidae; Sus.	
	primer_bind 1..18		REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Loofit,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P. and Chardon,P.	
	BASE COUNT 16 a 28 c 33 g 27 t 2 others		TITLE Variants of the gamma chain of ampk, dna sequences encoding the same, and uses thereof	
	ORIGIN QY_1121 ATCCCTGACTGGACATCTTGTGGACCCGGCTTGTCAGCTGGCTGTGGCT 106		JOURNAL Patent: WO 0120003-A 1 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR); Andersson, Leif (SE); Loofit, Christian (DE); Kalm, Ernst (DE)	
	Qy_281578 Sequence 1 from Patent WO0177305.		FEATURES Location/Qualifiers 1..1867	
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		DEFINITION 2 (bases 1 to 1873) AUTHORS Milan,D., Jeon,J.T., Loofit,C., Amarger,V., Robic,A., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., le Roy,P., Chardon,P. and Andersson,L.	
	AUTHORS Andersson,L.		TITLE A mutation in PRKG3 associated with excess glycogen content in pig skeletal muscle	
	DEFINITION Variants of the human ampk-activated protein kinase gamma 3 subunit		JOURNAL Science 288 (5469), 1248-1251 (2000)	
	ACCESSION WO 0177305-A 1 18-OCT-2001;		MEDLINE 20280150	
	VERSION AB (SE)		PUBMED 10818001	
	KEYWORDS		REFERENCE 2 (bases 1 to 1873) AUTHORS Milan,D., Jeon,J.T., Loofit,C., Paul,S., Gellin,J., Lundstrom,K., Reinsch,N., Gellin,P. and Andersson,L.	
	SOURCE		JOURNAL Direct Submission	
	ORGANISM Homo sapiens		TITLE Submitted (10-Dec-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suiidae; Sus.		JOURNAL University of Agricultural Sciences, BMC box 597, Uppsala 751 24,	
	REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Loofit,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., le Roy,P., Chardon,P. and Andersson,L.			
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	VERSION 1..1867			
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	REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Luthman,H. and Marlund,S.			
	DEFINITION Variants of the human ampk-activated protein kinase gamma 3 subunit			
	ACCESSION WO 0177305-A 1 18-OCT-2001;			
	VERSION AB (SE)			
	KEYWORDS			
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	ORGANISM Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suiidae; Sus.			
	REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Luthman,H. and Marlund,S.			
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	ACCESSION WO 0177305-A 1 18-OCT-2001;			
	VERSION AB (SE)			
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Luthman,H. and Marlund,S.			
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	VERSION AB (SE)			
	KEYWORDS			
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	ORGANISM Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suiidae; Sus.			
	REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Luthman,H. and Marlund,S.			
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	ACCESSION WO 0177305-A 1 18-OCT-2001;			
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	REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Luthman,H. and Marlund,S.			
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	ACCESSION WO 0177305-A 1 18-OCT-2001;			
	VERSION AB (SE)			
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suiidae; Sus.			
	REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Luthman,H. and Marlund,S.			
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	ACCESSION WO 0177305-A 1 18-OCT-2001;			
	VERSION AB (SE)			
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	ORGANISM Homo sapiens			
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	REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Luthman,H. and Marlund,S.			
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	ORGANISM Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suiidae; Sus.			
	REFERENCE 1 (bases 1 to 1867) AUTHORS Andersson,L., Luthman,H. and Marlund,S.			
	DEFINITION Variants of the human ampk-activated protein kinase gamma 3 subunit			
	ACCESSION WO 0177305-A 1 18-OCT-2001;			
	VERSION AB (SE)			
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suiidae; Sus.			
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	VERSION AB (SE)			
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	ACCESSION WO 0177305-A 1 18-OCT-2001;			
	VERSION AB (SE)			
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	ORGANISM Homo sapiens			

FEATURES Sweden
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BASE COUNT 382 a 580 c 535 g 376 t
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Search completed: January 7, 2003, 20:19:51
 Job time : 4648.03 secs

Result No.	Score	Query	Match	%	Length	DB	ID	Description
SUMMARIES								
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2	1372	83.3	2115	22	AAD03120	PRKAG3	CDNA,	Homo sapiens.
3	1366	82.9	2109	22	AAD03296	PRKAG3	inttron 2 -	Human AMP-activated protein kinase gamma 8
4	406	24.7	989	22	ABA08485	PRKAG3	inttron 2 -	Human AMP-activated protein kinase gamma 8
5	398	24.2	547	22	AAK72740	PRKAG3	inttron 10 -	Human immune/haema
c	7	278	16.9	1014	22	AAH43684	PRKAG3	inttron 4 -
c	8	252	15.3	3425	22	AAK72740	PRKAG3	inttron 10 -
c	9	168	10.2	1722	22	AAH43683	PRKAG3	inttron 4 -

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match	%	Length	DB	ID	Description
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2	1372	OLIGO_NUC	Gapop_60.0 , Gapext_60.0	83.3	2115	GenBank	AAH43685	Prkag3 gene, standard; cDNA; 1647 BP.
3	1366	Scoring table:	2185239 seqs, 1125999159 residues	82.9	2109	GenBank	AAH43685	Prkag3 gene, standard; cDNA; 1647 BP.
4	406	Perfect score	Word size : 15	24.7	989	GenBank	ABA08485	Prkag3 gene, standard; cDNA; 1647 BP.
5	398	Sequence:	Total number of hits satisfying chosen parameters: 6064	24.2	547	GenBank	AAK72740	Prkag3 gene, standard; cDNA; 1647 BP.
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No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PN	WO200177305-A2.							
XX	PD 18-OCT-2001.							
XX	XX							
PF	06-APR-2001; 2001WO-SE00765.							
XX	PR 07-APR-2000; 2000US-195665P.							
XX	PA (AREX-) AREXIS AB.							
XX	P1 Andersson L, Luthman H, Marklund S;							
XX	PT New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant -							
XX	DR WPI: 2001-657170/75.							
XX	P-PSDB: QQB47679.							
PS	PS Disclosure; Fig 5; 25bp; English.							
XX	This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320; resulting in the amino acid substitution p71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037; resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.							
SQ	Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;							
	Query Match 100 0%; Score 1647; DB 22; Length 1647;							
	Best Local Similarity 100 0%; Pred. No. 0;							
	Matches 1647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
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Db	1 TTGGCTGGGCTGCCACATGGGCCGGCTGGTGGAGCACGCACTGGCCAGAACCCCTTC 60							
Qy	61 CTGGAGCAGCTTGAGTGGGTTCTGAGCATAGAGTGGCTTCCTAGAGAAAGAACAG 120							
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Db	241 GGGGAAGCTCCGGTCAAGGCAAGCTGGTGGAGGAGGCACCAAGTGTCA 300							
Qy	301 CAAGACCAACCCCTGGCTCAAGCTGATCTGGGGGTGCACTCCACAAAGGGTC 360							
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Qy	361 GGACTGCCTCCCTGAGCTGATCTGGGGGTGCACTCCACAAAGGGTC 420							
Db	361 GGACTGCCTCCCTGAGCTGATCTGGGGGTGCACTCCACAAAGGGTC 420							
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Db	1561	CTTCATCTTCCCCACCCCATTTGCTGGTTCACTATGATTCAAGGTAGGGCTCTGCCCTG	1620	KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
Qy	1621	GGCCATGACACCCTCTTAGCTTC	1647	KW OS Homo sapiens.
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-MAY-2000 : 20000EP-0401388 .
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ANDERSSON L.
LOOFT C.
KALM E.
Lundström L., Loof C., Kalm E., Milan D., Robic A., Roge
Innunzelli N., Gellin J., Le Rov P., Chardon P.,
ALM/)

PI: 2001-244810/25.
PSDB; AAE00223.

aim 12: Page 65-68: 71 nn; English

The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKG3. Mutation in PRKG3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular disease, to modulate AMPK activity, and for restoring a normal AMPK function. PRKG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a generic polymorphic marker linked to a sequence encoding PRKG3 are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKG3. Transgenic animal and host cell transformed with PRKG3 or a

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Qy	1115	GCACCATCCTGACTGACTTGACATCTTGGACCCGGGTGTGTCCTGACTCTGTG	1174
Db	1021	GCACCATCCTGACTGACTTGACATCTTGGACCCGGGTGTGTCCTGACTCTGTG	1080
Qy	1175	GTCAGGAATGTTGTCAGGTGTCGGGCCCTATTCCTGGCTTTGATTCACTGGCT	1234
Db	1081	GTCAGGAATGTTGTCAGGTGTCGGGCCCTATTCCTGGCTTTGATGTTGATCACTGGCT	1140
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Db	1141	GCCCCGAAACCTTAACACCCTGGACATGAGTTGGAGAACGCCCTGGGGAGAACGACA	1200
Qy	1295	CTATCTCTGGAGGGAGTCTCTTCCAGGCCAACAGAGCTGGGGAAAGTGTGTCGAC	1354
Db	1201	CTATCTCTGGAGGGAGTCTCTTCCAGGCCAACAGAGCTGGGGAAAGTGTGTCGAC	1260
Qy	1355	AGGATCTGGGGAGCAGGTACACGGCTGTGTAGTGACGAGACCCAGCATCTTG	1414
Db	1261	AGGATCTGGGGAGCAGGTACACGGCTGTGTAGTGACGAGACCCAGCATCTTG	1320
Qy	1415	GGCGTGGTCTCCCTCTCCGACATCTTCAAGGACTGGTCTGCGCATCGAT	1474
Db	1321	GGCGTGGTCTCCCTCTCCGACATCTTCAAGGACTGGTCTGCGCATCGAT	1380
Qy	1475	GCCCTGGGGCTGAGAAGATCTGAGTCCTCAATCCCAAGCCA	1517
Db	1381	GCCCTGGGGCTGAGAAGATCTGAGTCCTCAATCCCAAGCCA	1423

Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other.
of PRKAG3 and is useful in gene therapy.

Query Match	Match	Score	DB	Length
Best Local Similarity	Similarity	1366	22	2109;
Matches 1416	Conservative	99 %	Pred. No.	0;
		Mismatches	Indels	Gaps
Y	101	TTCCTAGGAAAGAAAACAGCAGCTCATGCCATCACAGCTGTGACCAAGCAGCTCAGA	160	
b	1	TTCCTAGAAGAAAACGGGGCCAAAGCCTTCTGAGATGGACAAGGCCAGAACAGCTGGAG	60	
Y	161	AGAATCGTGGAAACGGGGCCAAAGCCTTCTGAGATGGACAAGGCCAGAACAGCTGGAG	220	
b	61	AGAATCGTGGAAACGGGGCCAAACGGTCAAGCTGAGATGGACAAGGCCAGAACAGCTGGAG	120	
Y	221	GAAGGGACCCACAGGTCAAGGGGAAGCTCCCGGGTCAAGGCCAGGTCTGAATGCCAC	280	
b	121	GAAGGGACCCACAGGTCAAGGGGAAGCTCCGGTCAAGGCCAACTGTCTGAATGCCAC	180	
Y	281	GGCTGGAGGCCACATTCCCCAGGACACACCCCTGGACTCAAGCTGATCTCCGGGGTG	340	
b	181	GGGTGGAGGCCACATTCCCCAGGACACACCCCTGGCTCAAGCTGATCTCCGGGGTG	240	
Y	341	GGCACTCCACCAACAGGGTGGACTGCTCCCTCTGACTGTACAGCCTCACTGAGGC	400	
b	241	GGCACTCCACCAACAGGGTGGACTGCTCCCTCTGACTGTACAGCCTCACTGAGGC	300	
Y	401	TCCAGCACAGATGATGTTGAGCTGGCAGGGTCTCCAGGCCAGGGCTGGACTGT	460	
b	301	TCCAGCACAGATGATGTTGAGCTGGCAGGGTCTCCAGGCCAGGGCTGGACTGT	360	
Y	461	GAACCTAGAGGGCTGTGAAAGAGGGCTGGCAGGGTCTCCAGGCCAGGGCTGGACTGT	520	
b	361	GAACCTAGAGGGCTGTGAAAGAGGGCTGGCAGGGCTGGACTGT	420	
Y	521	CCAAAGCTGGCTGGGATGAGCAACTGTGGGAAACCTGAGGGCTGGACTGT	580	

Db	421	CCCAGCTGGGATGAGAACTGGGATGAGAACTGGGCCCAAGATCPACATGGCCTTC	480	DT	21-JAN-2002	(first entry)
Qy	581	ATGCAGGAGCACACTGTCTGGATGCCAAGTGTCAAGCTAGTCATCTTCGAC	640	XX	PRKAG3	intron 2 - intron 4.
Db	481	ATGCAGGAGCACACTGTCTGGATGCCAAGTGTCAAGCTAGTCATCTTCGAC	540	DE	Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; KW metabolic disease; diabetes; obesity; substitution; db.	
Qy	641	ACCATGCTGGAGATCGAGGGCCTCTTGTCTGGTGCACGGCAGCC	700	XX	KW	
Db	541	ACCATGCTGGAGATCGAGGGCCTCTTGTCTGGTGCACGGCAGCC	600	OS	XX	
						Homo sapiens.
				FH	Key	Location/Qualifiers
				FT	intron	1..21
				FT		/*tag= a */number = "Intron 2"
				FT		/note = "3, portion of intron 2"
				FT	exon	22..177
				FT		/*tag= b */number = "Exon 3"
				FT	intron	178..541
				FT		/*tag= c */number = "Intron 3"
				FT	exon	542..945
				FT		/*tag= d */number = "Exon 4"
				FT	intron	946..989
				FT		/*tag= e */number = "Intron 4"
				FT		/note = "5, portion of intron 4"
				XX		
				PN		WO200177305-A2.
				XX		
				PD		18-OCT-2001.
				XX		
				PF		06-APR-2001; 2001WO-SE00765.
				XX		
				PR		07-APR-2000; 2000US-195665P.
				XX		
				PA		(AREX-) AREXIS AB.
				XX		
				PT		Andersson L, Luthman H, Marklund S;
				XX		
				DR		WPI ; 2001-657170/75.
				XX		
				PT		New variants of human AMP-activated protein kinase gamma 3 subunit
				PT		associated with a metabolic disease e.g. diabetes or obesity and method
				PT		for determining a risk estimate of diseases in subject by detecting the
				PT		variant -
				XX		
				PS		Example 1; Fig 2; 25pp; English.
				XX		
				CC		The sequences given in AAH41681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid
				CC		T for a C at nucleotide P71; in exon 4 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6.
				CC		
				SQ	Sequence 989 BP; 229 A; 306 C; 286 G; 168 T; 0 other;	
				Query Match	24.7%	Score 406; DB 22; Length 989;
				Best Local Similarity	100.0%	Pred. No. 3-5e-185; Mismatches 0; Indels 0; Gaps
				Matches 406;		
Qy	1481	GAGGCTGAGAAGATCTGACTCTCTCAATCTCCAAGCCA	1517	Qy	247	AGGTCGCCGCGTCCAGGCCAGCTGCTGTCACCCGCACTTCCCCAACAC 306
Db	1381	GGGGCTGAGAAGATCTGACTCTCTCAATCTCCAAGCCA	1417	Db	540	AGGTCGCCGCGTCCAGGCCAGCTGCTGTCACCCGCACTTCCCCAACAC 599
				RESULT 4		
				ID AAH43682		
				ID AAH43682 standard; DNA; 989 BP.		
				AC AAH43682;		
				XX		

Db 600 CACACCCCTGGCTCAAGCTGATTCCTGCCGGTGGACTCACCAACGGTGACTG 59
 Qy 367 CTCTCCCTCTGACTGTAGCCTGAGCTGAGATGTCAGTGAGCTGC 426
 Db 660 CTCTCCCTCTGACTGTAGCCTGAGCTCCAGCAAGATGATGTCAGTGAGCTGC 719
 Qy 427 CACGGAGTTCCACGCCACGAGGCTGGAGCTGAGCTGAGGAGCTGCTGAAGAG 486
 Db 720 CACGGAGTCCAGCCACAGGCTGGAGCTGAGGAGCTGCTGAAGAG 779
 Qy 487 GCGTGCCTGTCGCTGCTGTCGCCAGGGCCCATTCACAGCTGGCTGGATGACACT 546
 Db 780 GCGTGCCTGTCGCTGCTGTCGCCAGGGCCCATTCACAGCTGGCTGGATGACACT 839
 Qy 547 GCGGAAACCCGGGCCAGATCATGCGCTCATGGGACACCTGCTTACATGTC 606
 Db 840 GCGGAAACCCGGGCCAGATCATGCGCTCATACGCTTCATGAGGCTGACCTGCTACATGTC 899
 Qy 607 CATGGCAACTAGTCCAAAGCTCATCTTCGACACCATTGCTGGAG 652
 Db 900 CATGGCAACTAGTCCAAAGCTCATCTTCGACACCATTGCTGGAG 945

RESULT 5
ABA08485 standard; cDNA; 547 BP.

ABA08485;

XX

DT-11-JAN-2002 (first entry)

Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO:261.
 Human; cytokine; cell proliferation; cell differentiation; growth factor;
 haemopoiesis regulation; tissue immunomodulator; activin;
 inhibin; chemokines; chemokinesis; thrombolytic; oncogenesis;
 proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 chronic inflammatory condition; proliferative retinopathy;
 atherosclerosis; coronary heart disease; arterial ischaemia;
 bone disorder; osteoporosis; vascular growth disorder;
 tissue regeneration; wound healing; infection; immune disorder;
 cell culture; drug screening; gene therapy; antiinflammatory;
 antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 cytostatic; osteopathic; vasotropics; cardiotonic; viricide;
 antibacterial; antifungal; pulmonary; cardiotonic; antibiotic;
 ss-Homo sapiens.

XX

WO200157188-A2.

XX

PD-09-AUG-2001.

XX

PF-05-FEB-2001; 2001WO-US03800.

XX

PR-03-FEB-2000; 2000US-049694.

XX

PR-27-APR-2000; 2000US-0560875.

XX

(HYSEQ-) HYSEQ INC.

XX

Pi-Tang YT, Liu C, Drmanac RT;

XX

DR-WPI-2001-457740/49.

XX

DR-P-PSDB; ABB11241.

XX

sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haemopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activation or inhibition-related activities; chemokinetic receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haemopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.

Sequence 547 BP: 112 A; 172 C; 133 G; 130 T; 0 other;

Query Match 24.2%; Score 398; DB 22; Length 547;
 Best Local Similarity 100.0%; Pred. No. 2, 5e-18; Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 771 ATCGCTACTACAGTCCGCCCTGTCAGATCTATGAGATGGACAACTAAAGATTGAGA 830
 Db 34 ATCGCTACTACAGTCCGCCCTGTCAGATCTATGAGATGGACAACTAAAGATTGAGA 93
 Qy 831 CCTGAGGGAGATCTACCTGCAAGGCTGGCTCAAGCTCTGGCTCATCTCTCTATG 890
 Db 94 CCTGAGGGAGATCTACCTGCAAGGCTGGCTCAAGCTCTGGCTCATCTCTCTATG 153
 Qy 891 ATAGCTGTTGAGCTGCTTACCCCTATCAGAACGGATCTGGCTCATGCTGGCTGTTG 950
 Db 154 ATAGCTGTTGAGCTGCTTACCCCTATCAGAACGGATCTGGCTCATGCTGGCTGTTG 213
 Qy 951 TTGACCCGGTGTAGGCAACGTACTCCACATCTCACACAAACGCTGCTCAAGT 1010
 Db 214 TTGACCCGGTGTAGGCAACGTACTCCACATCTCACACAAACGCTGCTCAAGT 273
 Qy 1011 TGACACATCTTGGTCTCCGCTCCCTACCGACTATCCACATCTCACACAAACGCTGCTCAAGT 1070
 Db 274 TGACACATCTTGGTCTCCGCTCCCTACCGACTATCCACATCTCACACAAACGCTGCTCAAGT 333
 Qy 1071 TGGGATCGGACATTGGAGACTTGGCTGGCTGGAGAGCACCACCTGACTG 1130
 Db 334 TGGGATCGGACATTGGAGACTTGGCTGGCTGGAGAGCACCACCTGACTG 393
 Qy 1131 CACTGGACATCTTGGACAGCCTGGCTGGCTGGACTG 1168
 Db 394 CACTGGACATCTTGGACAGCCTGGCTGGCTGGACTG 431

AAH43684
 ID AAH43684 standard; DNA; 1014 BP.
 XX
 AC AAH43684;
 XX
 DT 21-JAN-2002 (first entry)
 XX
 DE PRKAG3 inttron 10 - 3' UTR.
 XX
 Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant;
 metabolic disease; diabetes; obesity; substitution; ds.
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FH intron 1..41
 FT /tag= a
 FT /number= "Intron 10"
 FT /note= "3' portion of intron 10"
 FT exon 42..79
 FT /tag= b
 FT /number= "Exon 11"
 FT intron 80..249
 FT /tag= c
 FT /number= "Intron 11"
 FT exon 250..396
 FT /tag= d
 FT /number= "Exon 12"
 FT intron 397..739
 FT /tag= e
 FT /number= "Intron 12"
 FT exon 740..856
 FT /tag= f
 FT /number= "Exon 13"
 FT 3' UTR 857..1014
 FT /tag= g
 PN WO200177305-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-SE00765.
 XX
 PR 07-APR-2000; 2000US-195665P.
 XX
 PA (ARXX-) AREXIS AB.
 XX
 PI Andersson L, Luthman H, Marklund S;
 XX
 WPI: 2001-657170/-75.
 XX
 PT New variants of human AMP-activated protein kinase gamma 3 subunit
 associated with a metabolic disease e.g. diabetes or obesity and method
 for determining a risk estimate of diseases in subject by detecting the
 PT variant -
 XX
 PS Example 1; Fig 4; 25pp; English.
 XX
 CC The sequences given in AAH43681-84 represent genomic fragments
 encoding the human AMP-activated protein kinase gamma 3 subunit
 (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant,
 CC is useful in determining a risk estimate of a metabolic disease,
 CC such as diabetes or obesity, in a subject. The variation may occur
 CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of
 CC a G for a C at nucleotide 320, resulting in the amino acid
 CC substitution P71A; in exon 4 variation may be a substitution of a
 CC T for a C at nucleotide 550; and in exon 10 variation may be a
 CC substitution of a T for a C at nucleotide 1037, resulting in the
 CC amino acid substitution R349W. There may also be nucleotide variation
 CC in intron 6.
 SQ Sequence 1014 BP; 192 A; 325 C; 271 G; 226 T; 0 other;

Query Match 16.9%; Score 278; DB 22; Length 1014;
 Best Local Similarity 100.0%; Pred. 0. 1Se-123; Missmatches 0; Indels 0; Gaps 0;

Qy 1370 CAGGTACAGGCTGGTCTAGTGACCAAGCCAGCATCTTGGGGGGTCTCCCTC 1429
 Db 737 CAGGTACAGGCTGGTCTAGTGACCAAGCCAGCATCTTGGGGGGTCTCCCTC 796
 Qy 1430 TCCGACATCTTCAGGCAGCTGGCTCAAGCCCTGCTGGCATGCCATGCGCTGCTGA 1489
 Db 797 TCCGACATCTTCAGGCAGCTGGCTCAAGCCCTGCTGGCATGCCATGCGCTGCTGA 856
 Qy 1490 GAAGATCTGAGTCCTCAATCCAAAGCCACCTGACACCTGGAAAGCCAATGAAGGAACTG 1549
 Db 857 GAAGATCTGAGTCCTCAATCCAAAGCCACCTGACACCTGGAAAGCCAATGAAGGAACTG 916
 Qy 1550 GAGAACCTGACCCCATTCATCTTCCCACCCATTGCTGTTAGCTATTCAGCTAG 1609
 Db 917 GAGAACCTGACCCCATTCATCTTCCCACCCATTGCTGTTAGCTATTCAGCTAG 976
 Qy 1610 GCCTGCCCCCTGGCCATGACACAGCCCTTAGTCTC 1647
 Db 977 GCCTGCCCCCTGGCCATGACACAGCCCTTAGTCTC 1014

RESULT 7
 AAK72740/c
 ID AAK72740 standard; DNA; 3425 BP.
 XX
 AC AAK72740;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27552.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01354.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180658.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186330.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-019076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-020515.
 PR 07-JUN-2000; 2000US-0209487.
 PR 28-JUN-2000; 2000US-0214986.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 04-FEB-2000; 2000US-0217880.
 PR 11-JUL-2000; 2000US-0217887.
 PR 14-JUL-2000; 2000US-0217896.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224118.
 PR 14-AUG-2000; 2000US-0224119.
 PR 14-AUG-2000; 2000US-0225123.
 PR 14-AUG-2000; 2000US-0225114.
 PR 14-AUG-2000; 2000US-0225166.
 PR 14-AUG-2000; 2000US-0225168.
 PR 14-AUG-2000; 2000US-0225170.
 PR 14-AUG-2000; 2000US-0225147.

PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-02256279.
 PR 22-AUG-2000; 2000US-0226581.
 PR 22-AUG-2000; 2000US-0226582.
 PR 23-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227099.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229487.
 PR 01-SEP-2000; 2000US-0229143.
 PR 01-SEP-2000; 2000US-0229144.
 PR 01-SEP-2000; 2000US-0229145.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0233143.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233013.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233105.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234224.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235048.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0235327.
 PR 29-SEP-2000; 2000US-0235367.
 PR 29-SEP-2000; 2000US-0236326.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241786.
 PR 08-NOV-2000; 2000US-0244674.
 PR 08-NOV-2000; 2000US-0244675.
 PR 08-NOV-2000; 2000US-0244676.
 PR 08-NOV-2000; 2000US-0244677.
 PR 08-NOV-2000; 2000US-0244678.
 PR 08-NOV-2000; 2000US-0244524.
 PR 08-NOV-2000; 2000US-0244525.
 PR 08-NOV-2000; 2000US-0244526.
 PR 08-NOV-2000; 2000US-0244527.
 PR 08-NOV-2000; 2000US-0244528.

PR 08-NOV-2000; 2000US-0244609.
 PR 08-NOV-2000; 2000US-0244610.
 PR 08-NOV-2000; 2000US-0244611.
 PR 08-NOV-2000; 2000US-0244613.
 PR 17-NOV-2000; 2000US-02449207.
 PR 17-NOV-2000; 2000US-02449209.
 PR 17-NOV-2000; 2000US-02449210.
 PR 17-NOV-2000; 2000US-02449211.
 PR 17-NOV-2000; 2000US-02449212.
 PR 17-NOV-2000; 2000US-02449213.
 PR 17-NOV-2000; 2000US-02449214.
 PR 17-NOV-2000; 2000US-02449215.
 PR 17-NOV-2000; 2000US-02449216.
 PR 17-NOV-2000; 2000US-02449217.
 PR 17-NOV-2000; 2000US-02449218.
 PR 17-NOV-2000; 2000US-02449244.
 PR 17-NOV-2000; 2000US-02449245.
 PR 17-NOV-2000; 2000US-02449264.
 PR 17-NOV-2000; 2000US-02449265.
 PR 17-NOV-2000; 2000US-02449277.
 PR 17-NOV-2000; 2000US-02449290.
 PR 01-DEC-2000; 2000US-02449300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251010.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251866.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251980.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA PA
 XX XX
 P1 Rosen CA, Barash SC, Ruben SM,
 XX XX
 DR WPI; 2001-483426/52.
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
 XX XX
 PS Disclosure; SEQ ID NO 27552; 3071pp + Sequence Listing; English.
 XX XX
 CC AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAK64702 to AAK91921. (I) have cytosolic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic genomic sequences from the present invention. AAK54912 to AAK51950 and AAK82169 represent sequences used in the exemplification of the present invention.
 CC Sequence 3425 BP; 916 A; 794 C; 951 G; 764 T; 0 other;
 SQ Query Match 15.3%; Score 252; DB 22; Length 3425;
 Best Local Similarity 100.0%; Pred. No. 5.1e-111;
 Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1396	CGAGGCCAGCATCTTGGCCTTCAGGCACTTCCGACATCTTCAAGGACTCTGGTGCT	1455
Db	3425	CGAGGCCAGCATCTTGGCCTTCAGGCACTTCCGACATCTTCAAGGACTCTGGTGCT	3366
Qy	1456	CAGCCCTGCTGGCATCGATGATGCCCTGGGGCTGAGAAGATCTGAGTCCTCAATCCAAAGC	1515
Db	3365	CAGCCCTGCTGGCATCGATGCCCTGGGGCTGAGAAGATCTGAGTCCTCAATCCAAAGC	3306
Qy	1516	CACCTGGCACACCTGGAGCCAATGAAGGAACTCGAGAACTCGAGACTCGCTCATTTCCCCA	1575
Db	3305	CACCTGGCACACCTGGAGCCAATGAAGGAACTCGAGAACTCGAGACTCGCTCATTTCCCCA	3246
Qy	1576	CCCCATTGTGGTTCACTGCTTCAAGGTTAGATTCTGGCTGGGCATGACCAAGC	1635
Db	3245	CCCCATTGTGGTTCACTGCTTCAAGGTTAGATTCTGGCTGGGCATGACCAAGC	3186
Qy	1636	CTCTTAGTCCTTC	1647
Db	3185	CTCTAGTCCTTC	3174
RESULT 8			
AAK72741/C			
ID	AAK72741	standard; DNA; 3425 BP.	
XX	XX		
AC	XX		
AAK72741;			
DT	06-NOV-2001	(first entry)	
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 27553.		
XX			
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cytostatic; gene therapy; vaccine; metastasis; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200157182-A2.		
XX			
PD	09-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US01354.		
XX			
PR	31-JAN-2000; 2000US-0179065.		
PR	04-FEB-2000; 2000US-0180628.		
PR	24-FEB-2000; 2000US-0184664.		
PR	02-MAR-2000; 2000US-0186350.		
PR	16-MAR-2000; 2000US-0189874.		
PR	17-MAR-2000; 2000US-0190076.		
PR	18-APR-2000; 2000US-0198123.		
PR	19-MAY-2000; 2000US-0205515.		
PR	07-JUN-2000; 2000US-0209467.		
PR	28-JUN-2000; 2000US-0214886.		
PR	30-JUN-2000; 2000US-0215135.		
PR	07-JUL-2000; 2000US-0216647.		
PR	07-JUL-2000; 2000US-0216880.		
PR	11-JUL-2000; 2000US-0217487.		
PR	11-JUL-2000; 2000US-0217496.		
PR	14-JUL-2000; 2000US-0218290.		
PR	26-JUL-2000; 2000US-0220963.		
PR	26-JUL-2000; 2000US-0220964.		
PR	14-AUG-2000; 2000US-0224518.		
PR	14-AUG-2000; 2000US-0224519.		
PR	14-AUG-2000; 2000US-0225213.		
PR	14-AUG-2000; 2000US-0225214.		
PR	14-AUG-2000; 2000US-0225266.		
PR	14-AUG-2000; 2000US-0225267.		
PR	14-AUG-2000; 2000US-0225268.		
PR	14-AUG-2000; 2000US-0225270.		
PR	14-AUG-2000; 2000US-0225447.		
PR	14-AUG-2000; 2000US-0225757.		
PR	14-AUG-2000; 2000US-0225758.		
PR	14-AUG-2000; 2000US-0226279.		

PR	17-NOV-2000; 2000US-0249207.	QY	1456	CAGCCCTCTGGCATCGATGCCCTGGGCTGAGAGATCTGAGTCATCCAAAGC 1515
PR	17-NOV-2000; 2000US-0249209.	Db	3325	CAGCCCTCTGGCATCGATGCCCTGGGCTGAGAGATCTGAGTCATCCAAAGC 3306
PR	17-NOV-2000; 2000US-0249210.	QY	1516	CACCTGC2ACACTGGGAACTGAGGAATCTGGCTTCACTCTCCCA 1575
PR	17-NOV-2000; 2000US-0249211.	Db	3305	CACCTGC2ACACTGGGAACTGAGGAATCTGGCTTCACTCTCCCA 3246
PR	17-NOV-2000; 2000US-0249212.	QY	1576	CCCCCATTGCGTTGAGTATTAGGTAGGGCTGGCATGACACCAGC 1635
PR	17-NOV-2000; 2000US-0249213.	Db	3245	CCCCCATTGCTGGTCACTGAGTATTAGGTAGGGCTGGCATGACACCAGC 3186
PR	17-NOV-2000; 2000US-0249214.	QY	1636	CTCTTAGCTTC 1647
PR	17-NOV-2000; 2000US-0249215.	Db	3185	CTCTTAGCTTC 3174
PR	17-NOV-2000; 2000US-0249216.			
PR	17-NOV-2000; 2000US-0249217.			
PR	17-NOV-2000; 2000US-0249218.			
PR	17-NOV-2000; 2000US-0249219.			
PR	17-NOV-2000; 2000US-0249220.			
PR	01-DEC-2000; 2000US-0249245.			
PR	01-DEC-2000; 2000US-0249246.			
PR	01-DEC-2000; 2000US-0249247.			
PR	01-DEC-2000; 2000US-0249248.			
PR	01-DEC-2000; 2000US-0249249.			
PR	01-DEC-2000; 2000US-0249250.			
PR	01-DEC-2000; 2000US-025016.			
PR	01-DEC-2000; 2000US-0250391.			
PR	05-DEC-2000; 2000US-0251030.			
PR	05-DEC-2000; 2000US-0251988.			
PR	06-DEC-2000; 2000US-0256719.			
PR	06-DEC-2000; 2000US-0251479.			
PR	08-DEC-2000; 2000US-0251856.			
PR	08-DEC-2000; 2000US-0251868.			
PR	08-DEC-2000; 2000US-0251899.			
PR	08-DEC-2000; 2000US-0251189.			
PR	11-DEC-2000; 2000US-0251990.			
PR	11-DEC-2000; 2000US-0254097.			
PR	05-JAN-2001; 2001US-0253678.			
XX	(HUMA-) HUMAN GENOME SCI INC.			
XX	Rosen CA, Barash SC, Ruben SM,			
XX	WPI: 2001-483426/52.			
XX	Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -			
PS	Disclosure: SEQ ID NO 27553; 3071pp + Sequence Listing; English.			
XX	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK7894 represent human immune/hematopoietic genomic sequences from the present invention. AAK54942 to AAM54950 and AAM82169 represent sequences used in the exemplification of the present invention.			
SQ	Sequence 3425 BP; 916 A; 794 C; 951 G; 764 T; 0 other;			
Query Match	15.3% ; Score 252; DB 22; Length 3425;			
Best Local Similarity	100.0% ; Pred. No. 5.1e-11;			
Matches 2x2;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	1396 CGAGACCCAGCATCTCTGGGCTGGTCTCCCTCCGACATCCTCAGGACTCTGGTCT 1455			
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	1042..1242			
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	1689..1722			
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/note= "5' portion of intron 10"
WO200177305-A2.
18-OCT-2001.
06-APR-2001; 2001WO-SE00765.
07-APR-2000; 2000US-195665P.
(AREX-) AREXIS AB.
Andersson L, Luthman H, Marklund S;
WPI; 2001-657170/75.
New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the variant -
Example 1; Fig 3; 25pp; English.

The sequences given in AAH43681-84 represent genomic fragments⁸ encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W.⁹ There may also be nucleotide variation

Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;
Intron: 6.

Query Match Score 168: DB 22; Length 1722;
 Best Local Similarity 100.0%; Pred. No. 1.5e-70;
 Marches 159. Conservative -

1042	GGTTCCCTGGCTGGCCCTCTTCCCTACCGCACTATCCAAGATTGCGCATGGC	1081
1523	GGTTCCCTGGCTGGCCCTCTTCCCTACCGCACTATCCAAGATTGCGCATGGC	1582
1082	ACATTCGGAGACTTGGCTGGTGTGGAGAGCAGCCCCATCTGACTGCACTGACATC	1141
1583	ACATTCGGAGACTTGGCTGGTGTGGAGAGCAGCCCCATCTGACTGCACTGACATC	1642

卷之三

1643 TTTGGACCCGGCTTGTCGCACTGCCCTGGTCAACGAATGTGGT 1690

3444706/C
3444711/1
3444715/1

ABA44706 standard; DNA; 378 BP.

ARA44706 :

U1-FEB-2002 (First entry)

Human breast cell single exon nucleic acid probe #3401.

Human: microarray; single; gene

disease; cancer; 68.

Homo sapiens

XX	30-JAN-2001;	2001WO-US00662.	
PF			
XX	04-FEB-2000;	2000US-0180312.	
PR	26-MAY-2000;	2000US-0207456.	
PR	30-JUN-2000;	2000US-0608408.	
PR	03-AUG-2000;	2000US-0234887.	
PR	21-OCT-2000;	2000US-0234887.	
PR	27-SEP-2000;	2000US-0236559.	
PR	04-OCT-2000;	2000GB-0024263.	
XX	(MOLE-) MOLECULAR DYNAMICS INC		
PA			
XX	Penn SG,	Hanzel DK,	Chen W,
PI			
XX	DR,		
XX	WPI;	2001-496933/54.	
PT	New spatially addressable set		
PT	useful for measuring gene expression		
PT	breast, comprises number of si		
XX	Claim 1; SEQ ID NO 3401; 327pp		
XX	CC The invention relates to a spatially		
CC	nucleic acid probes for measurement		
CC	from human breast and BT-473 cells		
CC	the probes with a collection of		
CC	derived from mRNA of human breast		
CC	bound to each probe of the microarray		
CC	verifying the expression of relevant		
CC	encode proteins. They are useful		
CC	determining predisposition and		
CC	expression analysis is useful		
CC	agents on cells. The microarray		
CC	diversity of probes for measurement		
CC	than expressed sequence tag microarray		
CC	rapid production of functional		
CC	present sequence is a single element		
CC	Note: The sequence data for the		
CC	printed specification, but was		
CC	from WIPO at ftp.wipo.int/pub/		
XX	Sequence 378 BP; 80 A; 128 C;		
Query Match	5-23%;	S	
Best Local Similarity	100.0%;		
Matches	85;	Conservative	
	0;		
Qy	651 AGATCAGAAAGCCCTCTTGTCT		
Db	351 AGATCAGAAAGCCCTCTTGTCT		
Qy	711 ACAGCAGAAAGCAGGTTGGGG		
Db	291 ACAGCAGAAAGCAGGTTGGGG		
RESULT	11		
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ID	ABA55162 standard;	DNA; 378 BP	
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AC			
XX			
DT	01-FEB-2002	(first entry)	
XX			
DE	Human foetal liver	single exon	
XX			
KW	Human; foetal liver; gene expression		
XX			
OS	Homo sapiens.		
XX			
PN	WO200157277-A2.		
XX			

XX	30-JAN-2001;	2001WO-US006662.
PF	04-FEB-2000;	2000US-0180312.
XX	26-MAY-2000;	2000US-0207456.
PR	30-JUN-2000;	2000US-0608408.
PR	03-AUG-2000;	2000US-0632366.
PR	21-SEP-2000;	2000US-0234487.
PR	27-SEP-2000;	2000US-0236559.
PR	04-OCT-2000;	2000GB-0024263.
XX	PA (MOLE-) MOLECULAR DYNAMICS INC	
XX	Penn SG,	Hanzel DK,
XX	Chen W,	
P1		
XX	DR	
XX	WPI:	2001-496933/54.
PT	New spatially-addressable set	
PT	useful for measuring gene expression	
PT	in breast, comprises number of sites	
XX	Claim 1; SEQ ID NO 3401;	327BP
PS	CC	The invention relates to a spatially
XX	CC	nucleic acid probes for measurement
CC	CC	from human breast and BT 474 cells
CC	CC	the probes with a collection of
CC	CC	derived from mRNA of human breast
CC	CC	bound to each probe of the microarray
CC	CC	verifying the expression of relevant
CC	CC	genes. They are useful for determining
CC	CC	expression analysis is useful
CC	CC	agents on cells. The microarray
CC	CC	diversity of probes for measurement
CC	CC	than expressed sequence tag microarray
CC	CC	rapid production of functional
CC	CC	present sequence is a single element
CC	CC	Note: The sequence data for the
CC	CC	printed specification, but was
CC	CC	from WIPO at ftp.wipo.int/pub/wipo/
XX	SQ	Sequence 378 BP; 80 A; 128 C;
Query Match	Best Local Similarity	5.2%
Matches	Matches	100.0%
85;	Conservative	0;
Qy	651	AGATCGAAAGGCCTTCCTTGCCTC
Db	351	AGATCGAAAGGCCTTCCTTGCCTC
Qy	711	ACAGCAAGAGGAGCTTGTGG
Db	291	ACAGCAAGAGGAGCTTGTGG
RESULT	11	
ABA55162/c	ID	ABA55162 standard; DNA; 378 BP
XX	AC	ABA55162;
XX	DT	01-FEB-2002 (first entry)
XX	DE	Human foetal liver single exon
XX	KW	Human; foetal liver; gene expression
XX	OS	Homo sapiens.
XX	PN	WO200157277-A2.
XX	YY	

CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
SQ Query Match 5.2%; Score 85; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 651 AGATCAAGAACGCCCTCTTGTCTGGTGCACAGGTGCGGGAGCCCTCTATGG 710
Db 351 AGATCAAGAACGCCCTCTTGTCTGGTGCACAGGTGCGGGAGCCCTCTATGG 292
Oy 711 ACAGCAAGAACAGAACGCTTTGGG 735
Db 291 ACAGCAAGAACAGAACGCTTTGGG 267

Search completed: January 6, 2003, 09:56:02
Job time : 329.832 secs

Result No.	Score	Query Match	Length	DB ID	Description
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2	6.8	4.1	485	1 W94830	BI344527 373008 MA
3	4.2	2.6	572	13 BI44527	AW356079 38073 MAR
4	4.1	2.5	399	10 AW356079	AW427435 63185 MAR
5	4.1	2.5	422	10 AW427435	BF890374 291826 MA
6	2.5	4.4	444	12 BF890374	

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OM nucleic - nucleic search, using sw model.

Run on: January 6, 2003, 09:44:42 ; Search time 2107.51 Seconds

(without alignments)
12656.598 Million cell updates /sec

Title: US-09-826-581-5

Pefect score: 1647

Sequence: 1 ttggcttggggctggccaca.....acaccagccctttatgtcttc 1647

Scoring table: OLIGO_NUC

Gapext 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 15

Total number of hits satisfying chosen parameters: 44986

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*

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1: em_estba:*
2: em_estbum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estzo:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_esttun:*
16: em_estrom:*
17: gb_gss:*
18: em_gss hum:
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fnn:*
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26: em_gss_pro:*
27: em_gss_rod:*
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RESULT 1

AA178898

LOCUS zp18d10_r1 Stratagene muscle 93/2209 Homo sapiens cDNA clone IMAGE:611731 5' similar to SW:AKG RAT P80385 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA CHAIN ; mRNA sequence.

AA178898

ACCESSION AA178898

VERSION 1

EST.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 413)

DEFINITION Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Scheibling,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Watson,R. and Wilson,R.

REFERENCE Unpublished (1997)

AUTHORS Contact: Wilson RK

IMAGE:611731 5'

PROTEIN KINASE, GAMMA CHAIN ; mRNA sequence.

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TITLE

JOURNAL

COMMENT

Washington University School of Medicine

4444 Forest Park Parkway, Box 6501, St. Louis, MO 63108

TeL: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Length: 1280 Std Error: 0.00

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Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 255.
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  SE COUNT
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		Indels	0;
		Gaps	0;
1121 ATCCGTGACTGGACATCTTGTGACCGCGCTGTGTGCAGTCGCTGTGGTCAAC	1180		
79 ATCCGTGACTGGACATCTTGTGACCGCGCTGTGTGCAGTCGCTGTGGTCAAC	138		
1181 GAATGGTCAAGGTCTGGGCTCTATTCCGGCTTGTATGTGATCCTGGTCCCCAG	1240		
139 GAATGGTCAAGGTCTGGGCTCTATTCCGGCTTGTATGTGATCCTGGTCCCCAG	198		
1241 CAAACCTACACCACTGGACATGAGTGGGGAGAGCCCTGGAG	1284		
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SULT 2						
44830						
CUS	w94830	485 bp	mRNA	EST	29-NOV-1996	
DEFINITION	ze3e10_r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone					
IMAGE:398890 5'						
W94830						
W94830.1						
EST.						
HUMAN						
ORGANISM						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	1 (bases 1 to 485)					
REFERENCE	Hillier,L., Clark,N., Dubroque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Ritkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,D., Wohldmann,P. and Wilson,R.					
TITLE	The WASU-Merck EST Project					
JOURNAL	Unpublished (1995)					
COMMENT	Unpublished (1995)					

Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 775 Std Error: 0.00
Seq Primer: mob.REGA+ET
High quality sequence stop: 431.
<http://locus.wustl.edu>

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/notc="Organ: heart Vector: pETT3D (Phage modified poly-linker Site 1: Not I; Site 2: Sma I) strand cDNA was primed with a Not I - Oligo TGTGACCAACTGAAAGTGCGAGGGCCGATCTTTTTTG double-stranded cDNA was size selected, adapters (Pharmacia), digested with Not I and Eco RI sites of a modified vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from same fetus as the fetal lung library, Soares_nbHH19W."
NbHH19W."
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BASE COUNT	ORIGIN
91 a	161 c
119 g	112 t
	2 other

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	Matches	Pred. NO.	1.9e-20;	;			
	0;	Mismatches	1;	Indels	0;	Gaps	0;
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Db 65	GAGAGATCTGAGCTTCAATCCAAAGCACCCTGCACACTGGAAAGCCATGAAAGGGAAC	124					
Qy 154B	TGGAAACTCAGCTTCAATTCTCCCCACCCCCATTTCGTGGTTAGCTATGATTCAAG	1606					
Db 125	TGGAAACTCAGCTTCAATTCTCCCCACCCCCATTTCGTGGTTAGCTATGATTCAAG	183					
RESULT 3							
BI144527	BI144527	572 bp	mRNA	linear	EST	30-JUL-2001	
LOCUS	373008 MARC 2PIG	Sus scrofa	cDNA 5'	mRNA	sequence.		
DEFINITION	373008 MARC 2PIG	Sus scrofa	cDNA 5'	mRNA	sequence.		
ACCESSION	BI144527						
VERSION	BI144527.1						
KEYWORDS	EST.						
SOURCE	pig.						
ORGANISM	Sus scrofa						
REFERENCE	Merazo, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.						
AUTHORS	Fahrkenburg, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grossie, W.M., Bennett, G.A., Laegreid, W.W., and Keele, J.W.						
TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine						
JOURNAL	Unpublished (2000)						
COMMENT	Contact: Smith TPL						
	USDA, ARS, US Meat Animal Research Center						
	Po Box 166, Clay Center, NE 68933-0166, USA						
	Tel: 402 762 4366						
	Fax: 402 762 4390						
	Email: smith@email.marc.usda.gov						
	Single pass sequencing. Bases called and alt trimmed with phred v0.980904. e. Vector identified by cross_match with the -minscore 18 and -minqual 12 options.						
	PCR Primers						
	FORWARD: AGCAAACAGCTATGCCAT						
	BACKWARD: GTTTTCCAGTCAGTCAGACG						
	Plate#: 119	row: 1	column: 11				
	Seq primer: ATTAGGTGACACTATAG.						
FEATURES	Location/Qualifiers						
source	1..572						

Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 106 a 190 c 151 g 124 t 1 others

BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Score	Length	mRNA	linear	EST
		Qy 1247 TACACCACTGGACATGAGTGTGGAGAAGGCCCTGAGCAG 1288	2.6%	Score 42; Pred. No. 2.4e-08;	Length 572;			25-APR-2001
		D _b 409 TACACCACTGGACATGACTGTGGAGAAGGCCCTGAGCAG 450	100.0% ; Conservative	0; Mismatches 0;	Indels 0;	Gaps 0;		
RESULT 4	AW356079	LOCUS	AM356079 MARC 2BOV Bos taurus	399 bp mRNA	EST 25-APR-2001			
		DEFINITION	AM356079	sequence.				
		VERSION	AM356079.1	GI:6600035				
		KEYWORDS	COW,					
		ORGANISM	Bos taurus					
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.					
		AUTHORS	1 (bases 1 to 422)					
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)					
		JOURNAL	Genome Res.	11 (4)	21180013	Contact: Smith TPL		
		MEDLINE	USDA, ARS, US Meat Animal Research Center	0	68933-0166, USA	USDA, ARS, US Meat Animal Research Center		
		COMMENT	Phone: 402 762 4390			Phone: 402 762 4390		
		FEATURES	source			Email: smith@email.marc.usda.gov		
		ORIGIN				Single pass sequencing. Bases called and trimmed with phred		
		DEFINITION				v0.980904 e. Vector identified by cross_match with the -minscore 20		
		VERSION				and -minmatch 12 options.		
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		ORGANISM	Bos taurus			FORWARD: AGGAACAGCTATGACCAT		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			BACKWARD: GTTTCCAGTGACGAGC		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			Plate: 32 row: F column: 22		
		AUTHORS	1 (bases 1 to 399)			Seq primer: ATTAGTCGACTATAG.		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			Location/Qualifiers		
		JOURNAL	Genome Res.	11 (4)	21180013	1. 422		
		MEDLINE	USDA, ARS, US Meat Animal Research Center	0	68933-0166, USA	/organism="Bos taurus"		
		COMMENT	Phone: 402 762 4390			/db_xref="taxon:9913"		
		FEATURES	source			/clone lib="MARC 3BOV"		
		ORIGIN				/tissue_type="pooled"		
		DEFINITION				/lab_host="DH10B"		
		VERSION				/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."		
		KEYWORDS	COW,			BASE COUNT	102 a	136 c 125 g 59 t
		ORGANISM	Bos taurus			Query Match	2.5%	Length 422;
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			Best Local Similarity	100.0%	Pred. No. 6.4e-08;
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			Matches	41;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		AUTHORS	1 (bases 1 to 422)			Qy 264 CAGCTCTGTCGTCACCGGGCTGGGCCATTCGGCCAG 304		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			Db 254 CAGCTCTGTCACCGGGCTGGGCCATTCGGCCAG 294		
		FEATURES	source			RESULT 6		
		ORIGIN				BF890374		
		DEFINITION				LOCUS	291826	MARC 3BOV Bos taurus CDNA 5', mRNA sequence.
		VERSION				DEFINITION	291826	MARC 3BOV Bos taurus CDNA 5', mRNA sequence.
		KEYWORDS	COW,			ACCESSION	BF890374	
		ORGANISM	Bos taurus			VERSION	BF890374.1	EST 25-APR-2001
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)			ACCESSION		
		FEATURES	source			VERSION		
		ORIGIN				KEYWORDS		
		DEFINITION				ORGANISM		
		VERSION				DEFINITION		
		KEYWORDS	COW,			ACCESSION		
		ORGANISM	Bos taurus			VERSION		
		MATERIALS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			KEYWORDS		
		REFERENCE	Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., Keele, J.W.			ORGANISM		
		AUTHORS	1 (bases 1 to 444)			DEFINITION		
		COMMENT	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)					

Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perteet,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980304.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRIMERS

FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCAGCTTCCAGTCAGCG
Plate: 90 row: I column: 16
Seq primer: ATTAGGTGACACTATAG.

FEATURES

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/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"

Query Match Score 41; DB 13; Length 548;
Best Local Similarity 100.0%; Pred. No. 6 8e-08;
Matches 41; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Library made from pooled tissue from testis, thymus,
semiterendinous muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

BASE COUNT 119 a 119 t 163 g 93 c

ORIGIN

Query Match Score 41; DB 13; Length 548;
Best Local Similarity 100.0%; Pred. No. 6 8e-08;
Matches 41; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semiterendinous muscle, and fetal
longissimus muscle.".

RESULT 8

LOCUS AW314499 298 bp mRNA linear EST 25-APR-2001

DEFINITION 10669 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION AW314499

VERSION AW314499.1 GI:6743764

EST.

KEYWORDS

BOS TAURUS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Bovidae; Cetartiodactyla; Ruminantia; Pecora; Bovidea.

1 (bases 1 to 298)

REFERENCE

AUTHORS Smith,T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perteet, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980304.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.

PCR PRIMERS

FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCAGCTTCCAGTCAGCG
Plate: 11 row: H column: 23
Seq primer: ATTAGGTGACACTATAG.

FEATURES

source

1. 298 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

COMMENT Contact: Smith TPL
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov

/lab host="DH10B"				
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;				
Library made from pooled tissue from marrow, alveolar				
macrophage, ovary, fetal semitendinosus muscle, and fetal				
longissimus muscle."				
55 a 96 c 81 g 66 t				
BASE COUNT	9			
ORIGIN				
Query Match				
Best Local Similarity	2.2%	Score 37; DB 10; Length 298;		
Matches 37; Conservative	100.0%; Pred. No. 4.2e-06;			
Mismatches 0; Indels 0;				
Gaps 0;				
REFERENCE				
AUTHORS	Cogburn, L.A. and Monsonego-Ornan, E.			
TITLE	ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and			
Project	Epiphyseal Growth Plate cDNA Library, USDA/IFAFS Animal Genome			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1335 Fax: 302-831-2822 Email: cogburn@udel.edu; www.chickest.udel.edu.			
FEATURES	Location/Qualifiers			
source	1. /organism="Gallus gallus" /strain="Commercial broiler and Ottawa Res. Centre Strains 90 & 21" /db_xref="taxon:9031;" /clone="Pm2n_pk005_j24" /clone_lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)" /sex="Male and Female" /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate" /dev_stage="Breast leg:Embryo(d19);post-hatch(lid,1,3,5,7,9 .11 weeks);growth plate(lid,7d,14d post-hatch)" /lab_host="E. coli PMDH10B" /note="vector: PCMVSPORT6; library made from equine pools of total RNA isolated from each tissue (embryonic muscle 31.3%, juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"			
BASE COUNT	126 a 199 c 137 g 133 t			
ORIGIN				
Query Match				
Best Local Similarity	1.5%; Score 24; DB 13; Length 95;			
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	737 ATGGTGTACATCACTGACTCATC 760			
Db	146 ATGGTGTACATCACTGACTCATC 169			
RESULT	11			
LOCUS	BG713637			
DEFINITION	mRNA linear EST 08-MAY-2001 pgm2n_pk008_c13 Normalized Liver Library Gallus gallus cDNA Clone pgm2n_pk008_c13' Similar to 91_04506 ref [NP_002724.1] protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gamma-1 [Homo sapiens] gi 12273789 ref [XP_006778_2]; protein kinase, AMP-activated, gamma 1 non, mRNA sequence			
ACCESION	BG713637			
VERSION	EST			
KEYWORDS				
SOURCE	chicken			
ORGANISM	Gallus gallus			
BUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI;				
ARCHOSAURIA; AVES; NEOGNATHAE; GALLIFORMES; PHASIANIDAE;				
PHASIANINAEE; GALLUS.				
1 (bases 1 to 595).				
REFERENCE				
AUTHORS	Burnside, J., Morgan, R.W. and Cogburn, L.A.			
TITLE	Unpublished (2001)			
PROJECT	Chicken ESTs from a normalized liver library			
RESULTS	10			
LOCUS	BM487789			
DEFINITION	mRNA linear EST 07-FEB-2002 pgm2n_pk005_j24 Normalized Chicken Breast Muscle, Leg Muscle, and			
Epiphyseal Growth Plate cDNA Library (pgm2n) Gallus gallus cDNA				
clone pgm2n_pk005_j24' similar to gb AAC52380.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus]				
, mRNA sequence.				

v0_980904.e Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PRIMERS
 FORWARD: AGAAAACAGCTATGACCAT
 BACKWARD: GTTTCAGTGACGACC
 Place: 40 row: O column: 13
 Seq primer: ATTAGGTGCACATAG.

FEATURES source
 Location/Qualifiers
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 /organism="Bos taurus"
 /db_xref="taxon:9613"
 /clone_lib="MARC 3BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from marrow, alveolar
 macrophage, ovary, fetal semitendinosus muscle, and fetal
 longissimus muscle."

BASE COUNT ORIGIN
 81 a 119 g 101 t
 173 c

Query Match
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1451 GTCCTCAGCCCTCTGGATCGA 1473
 Db 118 GTCCTCAGCCCTCTGGATCGA 140

RESULT 15

BI012981/_C LOCUS BI012981 124 bp mRNA linear EST 13-JUN-2001
 DEFINITION PM2-ET0206-160101-001-f08 ET0206 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BI012981
 VERSION BI012981.1
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 124)
 REFERENCE Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. J.F., Zago, M.A., Bordim, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.P., Matsumura, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT Contact: Simpson, A.J.G.

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research

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Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM2&t2=PM2-ET0206-160101-001-f08&t3=2001-01-16&t4=1>)

Seq primer: puc 18 forward
 High quality sequence start: 16
 High quality sequence stop: 124.

FEATURES source

Location/Qualifiers
 1. .124
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ET0206"
 /dev_stage="Adult"

/note="Organ: lung tumor; Vector: puc18; Site 1: Small;
 Site 2: Small; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent Application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the PUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions." BASE COUNT
 ORIGIN 30 a 26 c 43 g 25 t

Query Match
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1422 TCTCCCTCTCGGACATCCCTCA 1443
 Db 107 TCTCCCTCTCGACATCCCTCA 86

Search completed: January 6, 2003, 11:08:01
 Job time : 2115.51 secs


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FT    783..986
FT    /*tag= 9
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FT    987..1041
FT    /*tag= h
FT    /number= "Exon 8"
FT    1042..1242
FT    /*tag= i
FT    /number= "Intron 8"
FT    1243..1359
FT    /*tag= j
FT    /number= "Exon 9"
FT    1370..1572
FT    /*tag= k
FT    /number= "Intron 9"
FT    1523..1668
FT    /*tag= l
FT    /number= "Exon 10"
FT    1689..1722
FT    /*tag= i
FT    /number= "Intron 10"
FT    /note= "5' portion of intron 10"
XX WO2001177305-A2
PN XX
PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-SE000765.
XX PR 07-APR-2000; 2000US-195665P.
XX PA (AREXIS AB.
XX PI Andersson L, Luthman H, Marklund S;
XX WPI; 2001-657170/5.
XX
PT New variants of human AMP-activated protein kinase gamma3 subunit
PT associated with a metabolic disease e.g. diabetes or obesity and method
PT for determining a risk estimate of diseases in subject by detecting the
PT variant -
XX
PS Example 1: Fig 3: 25PP; English.
XX
CC The sequences given in AAH43681-84 represent genomic fragments
CC encoding the human AMP-activated protein kinase gamma 3 subunit
(CC (PRKG3). Detecting the presence of the PRKG3 DNA, or a variant,
CC is useful in determining a risk estimate of a metabolic disease,
CC such as diabetes or obesity, in a subject. The variation may occur
CC in exons 3, 4 or 10. In exon 3 variation may be a substitution of
CC a G for a C at nucleotide p71A, resulting in the amino acid
CC substitution P71A; in exon 4 variation may be a substitution of a
CC T for a C at nucleotide 550; and in exon 10 variation may be a
CC amino acid substitution R340W. There may also be nucleotide variation
CC in intron 6.
XX Sequence 1722 BP; 321 A; 504 C; 534 G; 363 T; 0 other;
XX
Query Match 100.0%; Score 1722; DB 22; Length 1722;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 CCTGGCCCTCAAGTCAAGAGGCCATGTCAGAGGCCTTGTGCTGAAACCGTGCGGAGC 60
DB 1 CCTGGCCCTCAAGTCAAGAGGCCATGTCAGAGGCCTTGTGCTGAAACCGTGCGGAGC 60
QY 1 CCTGGCCCTCAAGTCAAGAGGCCATGTCAGAGGCCTTGTGCTGAAACCGTGCGGAGC 60
QY 61 CCCTCTATGGACAGCAAGAAGCAGAGCTTGTGGCTGAGGAGGGCTGGAGGTGAAG 120
DB 61 CCCTCTATGGACAGCAAGAAGCAGAGCTTGTGGCTGAGGAGGGCTGGAGGTGAAG 120

```

Qy	1201	CTCCCTAAGCTGCCGAGGTCACTGCTCCCATCTCTGACGCCATCTCTGTTGAAGCTGTCATA	1260
Db	1201	CTCCCTAAGCTGCCGAGGTCACTGCTCCCATCTCTGAGCTGTTGAAGCTGTCATA	1260
Qy	1261	CACCTCATCAAGAACCGGATCCATGCCCTGCCCTGTCAGCGAACCTGAAACCTGCTT	1320
Db	1261	CACCTCATCAAGAACCGGATCCATGCCCTGCCCTGTCAGCGAACCTGAAACCTGCTT	1320
Qy	1321	ACTCCACATCCTCACACACAAACCCCTGCTCAAGTTCTGCACATCTTGTAAAGCTGGG	1380
Db	1321	ACTCCACATCCTCACACACAAACCCCTGCTCAAGTTCTGCACATCTTGTAAAGCTGGG	1380
Qy	1381	CCAGGTGGAGAAGGGAGACTGGCAGGTGATCAAGAGGGCTGAGGAGTCTTCAG	1440
Db	1381	CCAGGTGGAGAAGGGAGACTGGCAGGTGATCAAGGGCTGAGGAGTCTTCAG	1440
Qy	1441	CCCTTACGAGTCTGGGGAAAGAGCTGGAGCCCTCTTGAAGCTGCCCATCTCC	1500
Db	1441	CCCTTACGAGTCTGGGGAAAGAGCTGGAGCCCTCTTGAAGCTGCCCATCTCC	1500
Qy	1501	ACCTGGTCCCCATCTTAACTACGGGTTCCCTGTCGCCGCCCTCTTGAAGCTGGTCA	1560
Db	1501	ACCTGGTCCCCATCTTAACTACGGGTTCCCTGTCGCCGCCCTCTTGAAGCTGGTCA	1560
Qy	1561	TATCCAGATTTGGCATCGGACATTCGGAGACTTCGGTCTGGAGACAGACACC	1620
Db	1561	TATCCAGATTTGGCATCGGACATTCGGAGACTTCGGTCTGGAGACAGACACC	1620
Qy	1621	CATCCCTRACTGACTGGACATCTTGTGACCCGGGTGTGCTGCACTGGCTGTCATA	1680
Db	1621	CATCCCTRACTGACTGGACATCTTGTGACCCGGGTGTGCTGCACTGGCTGTCATA	1680
Qy	1681	CGAATGGTACCCACCCAGGATGAGGGCTGGCTGGA	1722
Db	1681	CGAATGGTACCCACCCAGGATGAGGGCTGGCTGGA	1722

RESULT 2

T 2				
700/C				
ABP44706 standard; DNA: 378 BP.				
ABP44706;				
01-FEB-2002 (first entry)				
Human; microarray; single exon nucleic acid probe #3401.				
HUMAN; disease; cancer; ss.				
Homo sapiens				
AG0200157271-A2.				
Db 302 CCCTATGGAGCAAGAAGGCTTGGTAGGAGGCTGGAGAG 243				
Qy 121 GGAGATGGAGGGGTGACGGTGTCTCGGTGATCTGTAT 180				
Db 242 GGAGATGGAGGGTGAACGGTGTCTGGTGTATCTGTAT 183				
Db 302 CCCTATGGAGCAAGAAGGCTTGGTAGGAGGCTGGAGAG 240				
Qy 181 ACCACAAGCTTGCCTTACGGGAGACTTCACATCCATCC 240				
Db 182 ACCACAAGCTTGCCTTACGGGAGACTTCACATCCATCC 123				
Db 302 CCCTATGGAGGAAACTTCACATCCATCCATCCATCC 300				
Qy 241 GGATCTGCATGCCAGCTGGAGACCTGGCTCAATTCCCACATCTGGAGGCCCT 300				
Db 122 GGATCTGCATGCCAGCTGGAGACCTGGCTCAATTCCCACATCTGGAGGCCCT 63				
Qy 301 ATGCCAGCTGACACCTTCACCTGGCTACTGCATGGCCTTGTC 346				
Db 302 CCCTATGGAGCAAGAAGGCTTGGTAGGAGGCTGGAGAG 243				

RESULT 3
 ABA55162/C
 ID ABA55162 standard; DNA; 378 BP.
 XX
 AC ABA55162;
 XX
 XX
 DT
 DB Human foetal liver single exon nucleic acid probe #3467.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 PD 09-Aug-2001.
 XX

useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
Claim 1; SEQ ID NO 3401; 327pp + sequence listing; English.

PF 30-JAN-2001; 2001WO-US00669.
 XX PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608108.
 PR 03-AUG-2000; 2000US-0612366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-483440/52.
 PT Human genome-derived single exon nucleic acid probes useful for
 analyzing gene expression in human fetal liver -
 XX PS Claim 1; SEQ ID NO 3467: 639pp + sequence listing; English.
 XX CC The invention relates to a single exon nucleic acid probe for
 measuring human gene expression in a sample derived from human foetal
 liver. The single exon nucleic acid probes may be used for predicting,
 measuring and displaying gene expression in samples derived from human
 fetal liver. The present sequence is a single exon nucleic acid
 probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at ftp://wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
 Query Match 20.1%; Score 346; DB 22; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.6e-148;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTGCCCTCAGATCAAGAAGCCCTCTTGGTGGCCAACGGTGTGGCGGCAGC 60
 Db 362 CCTGGCCCTCATCAGAAAGCCCTTGGTGGCCAACGGTGTGGCGGCAGC 303
 Qy 61 CCCCTCTATGGAGAGCAAGAACGAGCTTGTGGTGGAGGGCTGGTAGAAG 120
 Db 302 CCCCTCTATGGAGAGCAAGAACGAGCTTGTGGTGGAGGGCTGGTAGAAG 243
 Qy 121 GGAGATGGAGGGAGATTTACGGTTGTCTGGGCTGTCTGTGATAT 180
 Db 242 GGAGATGGAGGGAGATTTACGGTTGTCTGGGCTGTCTGTGATAT 183
 Qy 181 ACCAACAGCTTGGCTTCAAGCCAAGGCCAGCCAGGGCACAGGTGAGAACGTCATCC 240
 Db 182 ACCAACAGCTTGGCTTCAAGCCAAGGCCAGCCAGGGCACAGGTGAGAACGTCATCC 123
 Qy 241 GGAGTCAGTCAGCCAGCTGGAGACCTGGGTCAATTCCCCATCTGGAGGCCGT 300
 Db 122 GGAGTCAGTCAGCCAGCTGGAGACCTGGGTCAATTCCCCATCTGGAGGCCGT 63
 Qy 301 ATGACCAAGCTGACACCTTCACTCTGGCTACTGCAATGGCCCTGAGC 346
 Db 62 ATGACCAAGCTGACACCTTCACTCTGGCTACTGCAATGGCCCTGAGC 17
 RESULT 4
 ABA24907/_C
 ID ABA24907 standard; DNA; 378 BP.
 XX AC ABA24907;
 DT 23-JAN-2002 (first entry)
 XX DE Probe #3373 for gene expression analysis in human heart cell sample.
 XX KW Human; gene expression; heart; microarray; vascular system; probe;

KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 XX OS Homo sapiens.
 XX PN WO200157274-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US00666.
 XX PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608108.
 PR 03-AUG-2000; 2000US-0612366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488899/53.
 PT Single exon nucleic acid probes for analyzing gene expression in human
 hearts -
 PT hearts -
 XX PS Claim 1; SEQ ID NO 3373: 530pp; English.
 XX CC The present invention relates to single exon nucleic acid probes for
 measuring human gene expression in a sample derived from human heart. The
 present sequence is one such probe. The probes may be used for
 predicting, measuring and displaying gene expression in samples derived
 from the human heart via microarrays. By measuring gene expression, the
 probes are useful for predicting, diagnosing, grading, staging,
 monitoring and prognosis diseases of the human heart and vascular system
 e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp://wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
 Query Match 20.1%; Score 346; DB 22; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.6e-148;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTGCCCTCAGATCAAGAAGCCCTCTTGGTGGCCAACGGTGTGGCGGCAGC 60
 Db 362 CCTGGCCCTCATCAGAAAGCCCTTGGTGGCCAACGGTGTGGCGGCAGC 303
 Qy 61 CCCTCTATGGAGAGCAAGAACGAGCTTGTGGTGGAGGGCTGGTAGAAG 120
 Db 302 CCCTCTATGGAGAGCAAGAACGAGCTTGTGGTGGAGGGCTGGTAGAAG 243
 Qy 121 GGAGATGGAGGGAGATTTACGGTTGTCTGGGCTGTCTGTGATAT 180
 Db 242 GGAGATGGAGGGAGATTTACGGTTGTCTGGGCTGTCTGTGATAT 183
 Qy 181 ACCAACAGCTTGGCTTCAAGCCAAGGCCAGCCAGGGCACAGGTGAGAACGTCATCC 240
 Db 182 ACCAACAGCTTGGCTTCAAGCCAAGGCCAGCCAGGGCACAGGTGAGAACGTCATCC 123
 Qy 241 GGAGTCAGTCAGCCAGCTGGAGACCTGGGTCAATTCCCCATCTGGAGGCCGT 300
 Db 122 GGAGTCAGTCAGCCAGCTGGAGACCTGGGTCAATTCCCCATCTGGAGGCCGT 63
 Qy 301 ATGACCAAGCTGACACCTTCACTCTGGCTACTGCAATGGCCCTGAGC 346
 Db 62 ATGACCAAGCTGACACCTTCACTCTGGCTACTGCAATGGCCCTGAGC 17
 Query Match 20.1%; Score 346; DB 22; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.6e-148;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTGCCCTCAGATCAAGAAGCCCTCTTGGTGGCCAACGGTGTGGCGGCAGC 60
 Db 362 CCTGGCCCTCATCAGAAAGCCCTTGGTGGCCAACGGTGTGGCGGCAGC 303
 Qy 61 CCCTCTATGGAGAGCAAGAACGAGCTTGTGGTGGAGGGCTGGTAGAAG 120
 Db 302 CCCTCTATGGAGAGCAAGAACGAGCTTGTGGTGGAGGGCTGGTAGAAG 243
 Qy 121 GGAGATGGAGGGAGATTTACGGTTGTCTGGGCTGTCTGTGATAT 180
 Db 242 GGAGATGGAGGGAGATTTACGGTTGTCTGGGCTGTCTGTGATAT 183
 Qy 181 ACCAACAGCTTGGCTTCAAGCCAAGGCCAGCCAGGGCACAGGTGAGAACGTCATCC 240
 Db 182 ACCAACAGCTTGGCTTCAAGCCAAGGCCAGCCAGGGCACAGGTGAGAACGTCATCC 123
 Qy 241 GGAGTCAGTCAGCCAGCTGGAGACCTGGGTCAATTCCCCATCTGGAGGCCGT 300
 Db 122 GGAGTCAGTCAGCCAGCTGGAGACCTGGGTCAATTCCCCATCTGGAGGCCGT 63
 Qy 301 ATGACCAAGCTGACACCTTCACTCTGGCTACTGCAATGGCCCTGAGC 346
 Db 62 ATGACCAAGCTGACACCTTCACTCTGGCTACTGCAATGGCCCTGAGC 17
 RESULT 4
 ABA24907/_C
 ID ABA24907 standard; DNA; 378 BP.
 XX AC ABA24907;
 DT 23-JAN-2002 (first entry)
 XX DE Probe #3373 for gene expression analysis in human heart cell sample.
 XX KW Human; gene expression; heart; microarray; vascular system; probe;

RESULT 7

AAI13465/^C
ID AAI13465 standard; DNA; 378 BP.
XX
AC AAI13465;
XX DT 12-OCT-2001 (first entry)
DE Probe #3398 for gene expression analysis in human cervical cell sample.
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
cervical cancer; ss.
XX OS Homo sapiens.
XX PN WO200157278-A2.
XX PD 09-AUG-2001.
XX PR 30-JAN-2001; 2001WO-US00670.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0207456.
XX PR 03-AUG-2000; 2000US-063266.
XX PR 21-SEP-2000; 2000US-0236359.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-002463.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PS Claim 25: SEQ ID No 3398; 487pp; English.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX Note: the sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
SQ Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

AAI134821/c
ID AAI134821 standard; DNA; 378 BP.
XX AC AAI134821;
XX DT 17-OCT-2001 (first entry)
XX DE Probe #3507 used to measure gene expression in human placenta sample.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO00157272-A2.
XX PD 09-AUG-2001.
XX PR 30-JAN-2001; 2001WO-US00663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0207456.
XX PR 03-AUG-2000; 2000US-063266.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0234687.
XX PR 04-OCT-2000; 2000GB-002463.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0632366.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0234687.
XX PR 04-OCT-2000; 2000GB-002463.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-488897/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX Note: the sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;
SQ Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 20.1%; Score 346; DB 22; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGCCCTAGATCAAGAAGCCCTCTTGTGCTCTGGCTGCCAACGGTGTGGGGCAGC 60
Db 362 CCTGGCCCTAGATCAAGAAGCCCTCTTGTGCTCTGGCTGCCAACGGTGTGGGGCAGC 303

Qy 1 CCTGGCCCTCAAGATCAAGAGGCCCTTGTGTCACAGGGTGTGGGGCAGC 60
 Db 362 CCTGGCCCTCAAGATCAAGAGGCCCTTGTGTCACAGGGTGTGGGGCAGC 303
 Qy 61 CCTCTATGGACAGCAAGAGCAGAGCTTTGTGGTGAGGAGGGCTGGGTGAG 120
 Db 302 CCTCTATGGACAGCAAGAGCAGAGCTTTGTGGTGAGGAGGGCTGGGTGAG 243
 Qy 121 GGAGTGGAGGGATGGGGAGATCTGTACGGTTGTTGGCTGATCTGTAT 180
 Db 242 GGAGTGGAGGGATGGGGAGATCTGTACGGTTGTTGTGGCTGATCTGTAT 183
 Qy 181 ACCAAAGCTGGCTTCAAGCCAGGGCAGGGTGGAGAAAGTCCATCC 240
 Db 182 ACCAAAGCTGGCTTCAAGCCAGGGCAGGGTGGAGAAAGTCCATCC 123
 Qy 241 GGAGTCTGATGGCAGCTGGAGACCCTGGGCTCAATTTCCTCCATCTGTGAGGGCT 300
 Db 122 GGAGTCTGATGGCAGCTGGGACCCCTGGGCTCAATTTCCTCCATCTGTGAGGGCT 63
 Qy 301 ATGACAGCTGACACCTTACACTCCGCTACTGATGGCCCTGTGC 346
 Db 62 ATGACAGCTGACACCTTACACTCCGCTACTGATGGCCCTGTGC 17

RESULT 9
 AAI03344/C
 ID AAI03344 standard; DNA; 378 BP.
 XX
 AC AAI03344;
 DT 09-OCT-2001 (First entry)
 XX
 DE Probe #3335 used to measure gene expression in human breast sample.
 KW Probe; human; breast cancer; development disorder; ss;
 inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX
 Homo sapiens.
 XX
 WO20015270-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-US006661.
 XX
 PR 04-FEB-2000; 2000US-0160312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 03-AUG-2000; 2000US-0608408.
 PR 21-SEP-2000; 2000US-0632366.
 PR 04-OCT-2000; 2000US-0236359.
 PR 2000US-0034263.
 XX
 PA MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR; 2001-476286/51.
 XX
 PT Novel single exon nucleic acid probe used to measuring gene expression
 in a human breast -
 XX
 PS Claim 25; SEQ ID No 3335; 322pp; English.

CC include; breast cancer; disorders of development, inflammatory diseases
 CC of the breast, fibrocytic changes, proliferative breast disease and
 CC non-carcinoma tumours.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 Sequence 378 BP; 80 A; 128 C; 97 G; 73 T; 0 other;

Query Match 20-1%; Score 346; DB 22; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1..6..-148;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGCCCTCAAGATCAAGAGGCCCTTGTGGCTGTCAGGGCTGGGGCAGC 60
 Db 362 CCTGGCCCTCAAGATCAAGAGGCCCTTGTGGCTGTCAGGGCTGGGGCAGC 303
 Qy 61 CCTCTATGGACAGCAAGAGCAGAGCTTTGTGGTGAGGAGGGCTGGGTGAG 120
 Db 302 CCTCTATGGACAGCAAGAGCAGAGCTTTGTGGTGAGGAGGGCTGGGTGAG 243
 Qy 121 GGAGTGGAGGGATGGGGAGATCTGTACGGTTGTTGGCTGATCTGTAT 180
 Db 242 GGAGTGGAGGGATGGGGAGATCTGTACGGTTGTTGTGGCTGATCTGTAT 183
 Qy 181 ACCAAAGCTGGCTTCAAGCCAGGGCAGGGTGGAGAAAGTCCATCC 240
 Db 182 ACCAAAGCTGGCTTCAAGCCAGGGCAGGGTGGAGAAAGTCCATCC 123
 Qy 241 GGAGTCTGATGGCAGCTGGAGACCCTGGGCTCAATTTCCTCCATCTGTGAGGGCT 300
 Db 122 GGAGTCTGATGGCAGCTGGGACCCCTGGGCTCAATTTCCTCCATCTGTGAGGGCT 63
 Qy 301 ATGACAGCTGACACCTTACACTCCGCTACTGATGGCCCTGTGC 346
 Db 62 ATGACAGCTGACACCTTACACTCCGCTACTGATGGCCCTGTGC 17

RESULT 10
 ABS03407/C
 ID ABS03407 standard; DNA; 378 BP.
 XX
 AC ABS03407;
 XX
 DT 19-AUG-2002 (first entry)

XX Human genome-derived single exon probe from lung SEQ ID No 3398.
 XX
 DE Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangiomyomatosis; Karogenes syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 Homo sapiens.
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PR 30-JAN-2001; 2001WO-US00665.
 XX
 PR 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0236359.
 PR 2000US-0034263.
 XX
 PA MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR; 2001-476286/51.
 XX
 PT Novel single exon nucleic acid probe used to measuring gene expression
 in a human breast -
 XX
 PS Claim 25; SEQ ID No 3335; 322pp; English.

CC The present invention relates to novel single exon nucleic acid probes.
 CC The present sequence is one such probe. The probes are useful for
 CC measuring human gene expression in a human breast sample, where the probe
 CC hybridises at high stringency to a nucleic acid expressed in the human
 CC breast. The probes are useful for predicting, diagnosing, grading,
 CC staging, monitoring and prognosis of diseases of the human breast,
 CC particularly those diseases with polygenic aetiology. The diseases

XX	(MOLE-B) MOLECULAR DYNAMICS INC.	Db	182 ACCACAGCTGGCTTCAAGCCAGGGCAGGCCAAGCCCAGCCAGGGAAAGTCATCC	123
PA		Qy	241 GGAGTCGATGGCAACTGGGAGACTGTTCTGGCATCTGTGGACGCCCT	300
PI	Penn SG, Hantel DK, Chen W, Rank DR;	Db	122 GGAGTCGATGGCAACTGGGAGACTGTTCTGGCATCTGTGGACGCCCT	63
XX		Db	123 GTGGAGACCTGGGAGACTGTTCTGGCATCTGTGGACGCCCT	
DR	WPI: 2002-114183/15.	Qy	301 ATGACCAGCTGACACCTTCACTCCGTTACTCATGCCCTGTC	346
XX	Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -	Db	62 ATGACCAGCTGACACCTTCACTCCGTTACTCATGCCCTGTC	17
PT		SQ		
XX	Claim 1; SEQ ID No 3398; 634pp; English.	RES1		
XX	The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12367 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labelled nucleic acids derived from human lung mRNA, and (b), measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene comprising (a) identifying exons from genomic sequence by the method above and (b), measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to the exon, particularly microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberculous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemangiopericytoma, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocytic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and haline membrane disease. The present sequence is a single exon probe of the invention.	RES1		
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .	Query Match	20.1%; Score 346; DB 24; Length 378;	
CC	Sequence 378 BP; 80 A: 128 C: 97 G: 73 T: 0 other;	Best Local Similarity	100.0%; Pred. No. 1.6e-148;	
CC	SQ	Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DB	362 CCTGGCCCCCTAGATCAAGAGGCCCTTCTGGCTCTGGCAACGGCTGCGGCCAGC 60
XX		Qy	61 CCCTCTATGGACAGCAAGAGCAAGAGCTTGCGGAGCTGAGGGCTGGGGGTGAG 120	
DB	302 CCCTCTATGGACACCAAGAGCAAGAGCTTGCGGAGCTGAGGGCTGGGGGTGAG 243	Db	362 CCTGGCCCCCTAGATCAAGAGGCCCTTCTGGCTCTGGCAACGGCTGCGGCCAGC 180	
Qy	62 GGAGATGGAGGAGGTGAGGGAGATCTGGTGTGGGTGATCTCTGTAT 303	Db	242 GGAGATGGAGGAGGTGAGGGAGATCTGGTGTGGGTGATCTCTGTAT 183	
Qy	63 ACCAACAGCTGGCTTCAAGGCCAACGCCAGGGCCAGGGAGCTGGAG 240	Qy	121 GGAGATGGAGGAGGTGAGGGAGATCTGGTGTGGGTGATCTCTGTAT 180	

CC variation may be a substitution of a T for a C at nucleotide 1037, CC resulting in the amino acid substitution R340W. There may also be CC nucleotide variation in intron 6. The numbering of these CC variations is based on the full length cDNA as given, rather than on CC position 1 of the open reading frame.

XX Sequence 1647 BP; 346 A; 502 C; 462 G; 337 T; 0 other;

Query Match 9.8%; Score 168; DB 22; Length 1647;
Best Local Similarity 100%; Pred. No. 6e-7;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1022 GGTTCCTGTCGCCGGCCTCTACCGCACTATCAAAGATTGGCATGGC 1582
Qy 1523 GGTTCCTGTCGCCGGCCTCTACCGCACTATCAAAGATTGGCATGGC 1582
Db 1082 ACATTCGGAGACTGGCTGGTGGACTGCACTGGACATC 1642
Qy 1643 TTTGTGGACGGCTGGTGCTGTCGACTGGCTCAACGATGTGT 1690
Db 1142 TTGTGGACCGGGCTGGTGCTGTCGACTGGCTCAACGAAATGTGT 1189

RESULT 12

AAD03296 standard; DNA: 2109 BP.
XX AAD03296;

XX DT 13-JUN-2001 (first entry)

DE Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA.

XX Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK;
PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic;
genetic testing; carbohydrate metabolism disorder; skeletal muscle;
cystathione beta synthase; CBS; cardiant; gene therapy; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT 3' UTR 1..471 /*tag= b

FT 5' UTR 1..209 /*tag= a

CD5 472..1389 /*tag= a

FT 1..1390 /*tag= b
product= "Human Prkag3 protein"

XX WO200120003-A2.

XX PD 22-MAR-2001.

XX PP 11-SEP-2000; 2000WO-EPO9895.

XX PR 10-SEP-1999; 99EP-0402216.

XX PR 18-MAY-2000; 2000EP-0401388.

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(ANDE /) ANDERSSON L.

PA (LOOF /) LOOPT C.
(KALM /) KALM E.

XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX Iannuccelli N, Gellin J, Le Roy P, Chardon P;

DR WPI; 2001-244810/25.

XX PT New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders

XX PT P-PSDB; AA00221.

XX PT P-SEP-2000; 2000WO-EPO9896.

PT associated with energy metabolism such as diabetes, obesity, and myopathy -
XX PS Claim 12; Fig 2; 71pp; English.

CC The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases. To modulate AMPK activity, and for restoring a normal AMPK function, PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.

XX SQ Sequence 2109 BP; 458 A; 621 C; 560 G; 470 T; 0 other;	XX Query Match 9.8%; Score 168; DB 22; Length 2109;
XX AC Best Local Similarity 100.0%; Pred. No. 5.9e-67;	XX DT Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1523 GGTTCCTGTCGCCGGCCTCTACCGCACTATCAAAGATTGGCATGGC 1582	XX Db 922 GGTTCCTGTCGCCGGCCTCTACCGCACTATCAAAGATTGGCATGGC 1582
XX Qy 1583 ACATTCGGAGACTGGCTGGTGGACTGCACTGGACATC 1642	XX Qy 1583 ACATTCGGAGACTGGCTGGTGGACTGCACTGGACATC 1642
XX Db 1082 ACATTCGGAGACTGGCTGGTGGACTGCACTGGACATC 1141	XX Db 982 ACATTCGGAGACTGGCTGGTGGACTGCACTGGACATC 1041
XX Qy 1643 TTTGTGGACGGCTGGTGCTGTCGACTGGCTCAACGATGTGT 1690	XX Qy 1643 TTTGTGGACGGCTGGTGCTGTCGACTGGCTCAACGATGTGT 1690
XX Db 1142 TTGTGGACCGGGCTGGTGCTGTCGACTGGCTCAACGAAATGTGT 1089	XX Db 1042 TTGTGGACCGGGCTGGTGCTGTCGACTGGCTCAACGAAATGTGT 1089
XX RESULT 13	XX DT 13-JUN-2001 (first entry)
XX ID AAD03320 standard; cDNA; 2115 BP.	XX ID AAD03320
XX AC AAD03320;	XX AC AAD03320;
XX DT 13-JUN-2001	XX DT 13-JUN-2001
XX DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.	XX DE Human AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
XX KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.	XX KW Human; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; ss.
XX OS Homo sapiens.	XX OS Homo sapiens.
XX PH Key	XX PH Key
XX FT Location/Qualifiers	XX FT Location/Qualifiers
XX FT 1..471 /*tag= b	XX FT 1..471 /*tag= a
XX FT 1..209 /*tag= C	XX FT 1..1389 /*tag= C
XX CDS 472..1389 /*tag= a	XX CDS 1..1390 /*tag= a
XX FT product= "Human Prkag3 protein"	XX FT product= "Human Prkag3 protein"
XX FT 1..1390 /*tag= b	XX FT 1..1390 /*tag= b
XX XX	XX XX
XX PN WO200120003-A2.	XX PN WO200120003-A2.
XX PD 22-MAR-2001.	XX PD 22-MAR-2001.
XX PP 11-SEP-2000; 2000WO-EPO9895.	XX PP 11-SEP-2000; 2000WO-EPO9895.
XX PR 10-SEP-1999; 99EP-0402216.	XX PR 10-SEP-1999; 99EP-0402216.
XX PR 18-MAY-2000; 2000EP-0401388.	XX PR 18-MAY-2000; 2000EP-0401388.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.	PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (ANDE /) ANDERSSON L.	PA (ANDE /) ANDERSSON L.
PA (LOOF /) LOOPT C.	PA (LOOF /) LOOPT C.
PA (KALM /) KALM E.	PA (KALM /) KALM E.
XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;	XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;	XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
DR WPI; 2001-244810/25.	DR WPI; 2001-244810/25.
XX PT New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders	XX PT New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders
XX PT P-PSDB; AA00221.	XX PT P-PSDB; AA00221.
XX PT P-SEP-2000; 2000WO-EPO9896.	XX PT P-SEP-2000; 2000WO-EPO9896.
XX PT P-PSDB; AA00221.	XX PT P-PSDB; AA00221.
XX PN WO200120003-A2.	XX PN WO200120003-A2.
XX PD 22-MAR-2001.	XX PD 22-MAR-2001.
XX PP 11-SEP-2000; 2000WO-EPO9895.	XX PP 11-SEP-2000; 2000WO-EPO9895.
XX PR 10-SEP-1999; 99EP-0402216.	XX PR 10-SEP-1999; 99EP-0402216.
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PA (LOOF /) LOOPT C.	PA (LOOF /) LOOPT C.
PA (KALM /) KALM E.	PA (KALM /) KALM E.
XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;	XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;	XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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XX PT P-PSDB; AA00221.	XX PT P-PSDB; AA00221.
XX PN WO200120003-A2.	XX PN WO200120003-A2.
XX PD 22-MAR-2001.	XX PD 22-MAR-2001.
XX PP 11-SEP-2000; 2000WO-EPO9895.	XX PP 11-SEP-2000; 2000WO-EPO9895.
XX PR 10-SEP-1999; 99EP-0402216.	XX PR 10-SEP-1999; 99EP-0402216.
XX PR 18-MAY-2000; 2000EP-0401388.	XX PR 18-MAY-2000; 2000EP-0401388.
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PA (LOOF /) LOOPT C.	PA (LOOF /) LOOPT C.
PA (KALM /) KALM E.	PA (KALM /) KALM E.
XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;	XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;	XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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PA (KALM /) KALM E.	PA (KALM /) KALM E.
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XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;	XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;	XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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XX PP 11-SEP-2000; 2000WO-EPO9895.	XX PP 11-SEP-2000; 2000WO-EPO9895.
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PA (KALM /) KALM E.	PA (KALM /) KALM E.
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XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;	XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;	XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;	XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
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XX PD 22-MAR-2001.	XX PD 22-MAR-2001.
XX PP 11-SEP-2000; 2000WO-EPO9895.	XX PP 11-SEP-2000; 2000WO-EPO9895.
XX PR 10-SEP-1999; 99EP-0402216.	XX PR 10-SEP-1999; 99EP-0402216.
XX PR 18-MAY-2000; 2000EP-0401388.	XX PR 18-MAY-2000; 2000EP-0401388.
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PA (KALM /) KALM E.	PA (KALM /) KALM E.
XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;	XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;	XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
DR WPI; 2001-244810/25.	DR WPI; 2001-244810/25.
XX PT New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders	XX PT New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders
XX PT P-PSDB; AA00221.	XX PT P-PSDB; AA00221.
XX PN WO200120003-A2.	XX PN WO200120003-A2.
XX PD 22-MAR-2001.	XX PD 22-MAR-2001.
XX PP 11-SEP-2000; 2000WO-EPO9895.	XX PP 11-SEP-2000; 2000WO-EPO9895.
XX PR 10-SEP-1999; 99EP-0402216.	XX PR 10-SEP-1999; 99EP-0402216.
XX PR 18-MAY-2000; 2000EP-0401388.	XX PR 18-MAY-2000; 2000EP-0401388.
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PA (ANDE /) ANDERSSON L.	PA (ANDE /) ANDERSSON L.
PA (LOOF /) LOOPT C.	PA (LOOF /) LOOPT C.
PA (KALM /) KALM E.	PA (KALM /) KALM E.
XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;	XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Gaillard C;
XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;	XX PI Iannuccelli N, Gellin J, Le Roy P, Chardon P;
DR WPI; 2001-244810/25.	DR WPI; 2001-244810/25.
XX PT New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders	XX PT New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders
XX PT P-PSDB; AA00221.	XX PT P-PSDB; AA00221.
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PA (ANDE /) ANDERSSON L.	PA (ANDE /) ANDERSSON L.
PA (LOOF /) LOOPT C.	PA (LOOF /) LOOPT C.
PA (KALM /) KALM E.	PA (KALM /) KALM E.
XX PI Andersson L, Loopt C, Kalm E, Milan D, Robic A, Rogel-Ga	

PR 10-SEP-1999; 99EP-0402336.
 PR 18-MAY-2000; 2000EP-0401388.
 XX
 PA (INRG) INRA INST NAT RECH AGRONOMIQUE .
 PA (ANDE/) ANDERSSON L.
 PA (LOOF/) LOOFT C.
 PA (KALM/) KALM E.
 XX
 PI Andersson L, Looft C, Kalm E, Milan D, Robic A, Rogel-Gaillard C,
 PI Iannucelli N, Gellin J, Le Roy P, Chardon P,
 XX
 DR WPI: 2001-244810/25.
 DR P-PSDB; AAE0023.
 XX
 PS Claim 12: Page 65-68; 71pp. English.
 XX
 CC The present sequence is a cDNA encoding human adenosine monophosphate
 CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
 CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of
 CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
 CC useful as therapeutic for treating carbohydrate metabolism disorders such
 CC as diabetes, obesity, and disorders associated with muscle metabolism
 CC such as myopathy and cardiovascular diseases, to modulate AMPK
 CC activity, and for restoring a normal AMPK function. PRKAG3 sequence
 CC and its functionally altered mutants are useful for the diagnostic
 CC evaluation, genetic testing and prognosis of a metabolic disorder,
 CC preferably a carbohydrate metabolism disorder. Primers that can detect
 CC a genetic polymorphic allele linked to a sequence encoding PRKAG3, are
 CC useful for detecting a dysfunction of carbohydrate metabolism resulting
 CC from the expression of a functionally altered allele of PRKAG3.
 CC Transgenic animal and host cell transformed with PRKAG3 or a
 CC heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for
 CC screening compounds able to modulate AMPK activity. Nucleic acid
 CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
 CC in a sequence encoding the first cystathione beta synthase (CBS) domain
 CC of PRKAG3 and is useful in gene therapy.
 XX
 SQ Sequence 2115 BP; 460 A; 622 C; 562 G; 471 T; 0 other;
 Query Match 9.9%; Score 168; DB 22; Length 2115;
 Best Local Similarity 100 %; Pred. No. 5.9e-67;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1523 GGTTCCCTGTGCCGGCTCTTCCCTACCGACTATCCAAGATTGGCATGGC 1582
 Db 928 GGTTCCCTGTGCCGGCTCTTCCCTACCGACTATCCAAGATTGGCATGGC 987
 Oy 1583 ACATCCGAGACTGGCTGGAGACGACCATCCCTGACTGGACATC 1642
 Db 988 ACATCCGAGACTGGCTGGAGACGACCATCCCTGACTGGACATC 1047
 Oy 1643 TTGTGGACGGCTGGACTGGCTGTCACGAAATGGTGT 1690
 Db 1048 TTGTGGACGGCTGGACTGGCTGTCACGAAATGGTGT 1095
 RESULT 14
 ID ABA08485 standard; cDNA; 547 BP.
 XX
 AC ABA08485;
 XX DT 11-JAN-2002 (First entry)
 XX DE Human AMP-activated protein kinase subunit homologue cDNA, SEQ ID NO: 261.
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematoopoiesis regulation; tissue growth; immunomodulator; activin;

KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KW metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW gene; drug screening; antiinflammatory; gene therapy;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteoplastic; vasotropic; cardiotonic; viricide; ss;
 KW antifungal; pulmonary; antiulcer; antibiotic;
 XX
 OS Homo sapiens.
 XX
 PN WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US03800.
 XX
 PR 03-FEB-2000; 2000US-0496314.
 PR 27-APR-2000; 2000US-0560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT,
 XX
 DR WPI: 2001-457740/49.
 DR P-PSDB; ABB11241.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX
 PS Claim 1: Page 429; 1961pp; English.
 XX
 CC Sequences ABB10981-ABB12340 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09570 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC hematoopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activities; haemostatic, thrombotic or
 CC chemokinetic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis; cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or rheumatitis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC which can be used to augment or replace cells damaged by illness.
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 CC novel human polypeptide of the invention.

XX Sequence 547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;

XX Query Match 8.5%; Score 147; DB 22; Length 547;

Best Local Similarity 100.0%; Pred. No. 2.8e-57;

Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1523 GGTTCCTGCTGCCGGCCCTCCTACCGACTATCCAGATTGGCCATCGGC 1582

Db 285 GGTTCCCTGCTGCCGGCCCTCCTACCGACTATCCAGATTGGCCATCGGC 344

Qy 1583 ACATTCGGAGACTTGGCTGGTGAGACGCCCATCCCTGACTGGACATC 1642

Db 345 ACATTCGGAGACTTGGCTGGTGAGACGCCCATCCCTGACTGGACATC 404

Qy 1643 TTGTGGACCGGGCTGTCTGACTG 1669

Db 405 TTGTGGACCGGGCTGTCTGACTG 431

RESULT 15

ABA9850/C

ID ABA9850 standard; DNA; 92 BP.

XX AC ABA9850;

XX DT 01-FEB-2002 (first entry)

XX DE Human breast cell single exon nucleic acid probe #8545.

XX KW Human; microarray; single exon probe; gene expression; breast;

XX disease; cancer; ss.

OS Homo sapiens.

XX PN WO200157271-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US006662.

XX PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0216359.

PR 04-OCT-2000; 2000US-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR 2001-496933/54.

XX New spatially addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -

XX Claim 4; SEQ ID NO 8545; 327pp + sequence listing; English.

XX The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contracting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode Proteins. They are useful for gene discovery, and for determining predisposition and/or diagnosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias

CC than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC SQ Sequence 92 BP; 22 A; 24 C; 34 G; 12 T; 0 other;

Query Match 3.8%; Score 65; DB 22; Length 92;

Best Local Similarity 100.0%; Pred. No. 1.3e-19;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGGCCCTCGATCAAGAAGGCCCTCTGCTCGGTGGCAAGGTGTCGGGCAGC 60

Db 65 CCTGGCCCTCGATCAAGAAGGCCCTCTGCTCGGTGGCAAGGTGTCGGGCAGC 6

Qy 61 CCCTC 65

Db 5 CCCTC 1

Search completed: January 6, 2003, 09:55:47

Job time : 336.168 secs